A comparison of between-tree competition effects in separate stands of a *Eucalyptus grandis* seedling and a single *Eucalyptus grandis x urophylla hybrid clone*.

A DISSERTATION SUBMITTED TO THE FACULTY OF SCIENCE, UNIVERSITY OF THE WITWATERSRAND, JOHANNESBURG, IN FULFILLMENT OF THE REQUIREMENTS FOR THE DEGREE MASTER OF SCIENCE.

SUBMITTED BY: GIOVANNI SALE
PIETERMARITZBURG 2005

DECLARATION

I declare that this dissertation is my own, unaided work. It is submitted for the Degree of Master of Science in the University of the Witwatersrand, Johannesburg. It has not been submitted before for any degree or examination in any other University.

_____

_____ day of _____2005

ABSTRACT

The effect of between-tree competition in separate even aged stands of a *Eucalyptus grandis* seedling and a single *Eucalyptus grandis x Eucalyptus urophylla* hybrid clone was assessed. This was done by comparing treatments within an experiment, that was designed to test the effect planting density and genotype had on timber production and stand dynamics through time. This experiment is located on an escarpment in the Summer rainfall region of South Africa, approximately 7 km North West of Albert Falls dam in the Kwa-Zulu Natal Midlands. The terrain is flat with deep apedal soils, and the site has an estimated mean annual precipitation of 1143 mm. The simplest method of evaluating competition effects in plantation stands is through the use of spacing trials. Spacing trials create stands/plots in which all silvicultural and climatic variables are constant. Differences between treatments can then be attributed to competition alone. The planting densities tested were 6667 stems.ha^{-1}, 3333 stems.ha^{-1}, 2222 stems.ha^{-1}, 1587 stems.ha^{-1} and 1111 stems.ha^{-1} respectively. Competition was measured at three levels, namely; (i)individual tree, (ii)size-class and (iii)stand level. Vigour and its distribution within the population were used to explain competition processes. Basal area was chosen as the size variable for which vigour would be analysed. Relative Growth Rate (RGR) and Relative Production Rate (RPR) were chosen as the measures of vigour for analysis. Morphological changes in the trees as a result of competition were also used to understand the competitive mechanisms. It was found that resources are not shared amongst individuals in proportion to their size, but rather the larger individuals use disproportionately more of the resources than the smaller individuals, and therefore competition is asymmetrical. The dominant form of competition was found to be resource pre-emption where larger individuals passively prevent solar resources from reaching smaller competitors. Using RPR as the measure of vigour, competition was found to be one-sided, meaning that smaller individuals do not reduce the vigour of larger ones. If RGR is accepted as the measure of vigour then competition is two-sided meaning that the smaller individuals do reduce the vigour of the larger ones to a certain extent. There was no difference in the degree to which the smaller competitors in the clonal and seedling treatments reduced the growth of the larger individuals. The self-thinning rate in the seedling treatments was significantly higher than in the clonal treatments. Increases in mean tree size and production per hectare were accompanied by increases in mortality in the seedling treatments. In the clonal treatments it was found that even once the mean tree size approached the self thinning line, very few or no trees died, however there was also very little or no increase in mean tree size. When the relationship between number of live trees and production per hectare was analysed it was found that the clone could increase production per hectare without any change in survivorship, which is contrary to popular theory. As time progressed the skewness of the population progressed from negative to positive. This increase was the most pronounced in the higher planting density treatments, and the clonal treatments. The size variability in the population first decreased, then steadily increased. This increase was more pronounced in the high planting density treatments, and the clonal treatments. Clones and seedlings react in very different ways to competition. The large differences in population dynamics observed, indicate that we cannot just apply knowledge built up over the years regarding the management of *Eucalyptus grandis* and other plantation species to *Eucalyptus* hybrid clones.

DEDICATION

I dedicate this to my wife Sara and daughter Gabriella, whom have had to take a back seat at times, while I have been working on this dissertation. I further dedicate this to my parents, as without their encouragement I would never have completed this document. This is for you.

ACKNOWLEDGEMENTS

I would like to thank the following for their part in making this work possible:

- Professor Mary Scholes (Supervisor) for her advice, support and funding;
- Professor Sune Linder (Co-supervisor) for his advice;
- Leander Jarvell and Rob Pallet for planting the experiment;
- Desmond Ndlovu for his field work, trial maintenance, data collection and data capture;
- Dr Andrew Morris and Rob Pallet for their advice and encouragement;
- Sappi for allowing me to use their data for the completion of this work.
- NRF for funding;

Table of Content

TABLE OF APPENDICES

LIST OF FIGURES

List of Tables

Chapter 1. Introduction

There is currently ± 1.5 million ha of land apportioned to plantation forestry in South Africa, comprising 1.3 % of the total surface area. Pulpwood constitutes 68.7% of the total round-wood intake by the primary processing sector. In 1996/1997 the contribution of the forestry industry to the gross value of agricultural output was 7.3%. Between 1995 and 1997 49.7% of all new afforestation was to *Eucalyptus spp*. New afforestation decreased from ±3% annum^{-1} in 1990/1991 to 0.75% annum^{-1} in 1996/1997 (FOA, 1998). This reduction is a result of government legislation and the arid nature of South Africa. In order to increase *Eucalyptus* pulpwood production in South Africa, there is a need to increase the productivity of existing plantations.

Several strategies used alone or in combination can be employed to improve production from afforested land.
Improved risk control: Risks include fire, drought, hail, frost, disease and pests. The main risk control strategy currently used is matching species to site, and in so doing increase productivity.
Improved silviculture: By improving site preparation, planting practice, fertilisation and weed-control techniques, production can be increased.
Tree breeding: Tree breeding results in continuous genetic improvement. There are various deployment strategies available for this improved genetic material, which result in varying levels of improved production. The deployment of clonal material represents the greatest possible gain from any tree-breeding programme.
Regime manipulation: Manipulation of the management regime, by using different rotation lengths and/or planting densities on different sites, can result in significant production increases.

Certain plantations are inherently more productive than others. This can be as a result of management practice, however it is usually a function of soil and climatic factors. The largest productivity increases are likely to occur on the best quality sites. For this reason it is on these sites that the best genetic material is planted and management regimes manipulated most frequently. A large portion of the clonal material produced in South Africa is planted on the best quality sites e.g. the Zululand coast. Rotation lengths are generally shorter due to faster growth, with higher planting densities being investigated due to the higher carrying capacity of these good sites. With the faster growth and increased planting densities encountered on good quality sites, between-tree competition would be expected to set in sooner than on other sites. Understanding the competitive effects in clonal and seedling stands is therefore relevant to management if the production per unit area of land is to be increased.

Chapter 2. Literature Review

2.1. Definition of Competition

"Competition is an interaction between individuals, brought about by a shared requirement for a resource in limited supply, and leading to a reduction in the survivorship, growth and/or reproduction of the competing individuals concerned" (Begon *et al*. 1990).

Encyclopedia.com defines competition in biology as " the relationship between members of the same or different species in which individuals are adversely affected by those having the same living requirements, such as food or space. *Merriam-Webster Collegiate Dictionary* defines competition as "active demand by two or more organisms or kinds of organisms for some environmental resource in short supply".

2.1.1. Inter-specific vs. Intra-specific competition.

Merriam-Webster Collegiate Dictionary defines intra-specific as "occurring within a species or involving members of one species" and inter-specific as "existing, occurring, or arising between species".

Therefore by combining Inter/Intra- specific with competition we get the following definitions:

Encyclopedia.com defines intra-specific competition as "competition among members of the same species" and inter-specific competition as " competition among members of different species for the same ecologically limiting factors".

Inter-specific is when individuals of one species experience a reduction in growth and survivorship as a result of resource exploitation or interference by individuals of another species (Begon *et al*. 1990). Individuals of the same species have very similar requirements for survival and growth; but their combined demand for a resource may exceed the immediate supply. The individuals then compete for the resource and at least some of them become deprived. Intra-specific competition leads to decreased rates of resource intake per individual, decreased rates of individual growth, decreases in amounts of stored reserves or to increased risk of disease infection. These may lead in turn to increased mortality (Begon *et al*. 1990).

Von Euler *et al.* (1992) suggested that competitive process among several genotypes could be considered in terms of severity, symmetry and specificity. Severity is the degree to which a resource competed for is limiting biomass growth. Competition is symmetric if a scarce resource is utilized by competing neighbours in proportion to their size, but asymmetric if, say, the larger neighbours obtain disproportionately more resource (West *et al*. 1989 as cited by Von Euler *et al*. 1992). Specificity is the degree to which the competitive neighbourhood is genetically fixed.

2.1.2. Intra-genotypic competition vs. Intra-specific competition.

Inter-genotypic competition is the competition between two or more organisms, which are genetically dissimilar, for limited resources. Intra-specific competition is a form of inter-genotypic competition. Intra-genotypic competition is when two or more organisms with identical genes (ramets of a clone) compete for limited resources. Fasoula and Fasoula (1997) state that plants can be grown in three simple ecosystems, namely: (1) Isolation environment, where widely spaced plants exclude plant-to-plant interference (i.e. They do not compete for resources); (2) The competition environment, composed of interactions of genetically dissimilar genotypes (this includes both inter- and intra-specific competition); (3) The crop environment, composed of interactions between genetically identical genotypes (i.e. Competition between ramets of the same clone (Intra-genotypic competition)). Therefore plantation forest trees deployed as seedlings will interact in a competition environment and trees deployed as clonal cuttings (and planted as mono-clonal plots) will interact in a crop environment.

Competition is keenest amongst genetically identical plants, and by making nearly the same demands on the habitat, they adjust with difficulty to their mutual interactions (Clements *et al*. (1929) *ex Fasoula and Fasoula 1997*). Competition is intense due to acquired dissimilarity in growth and development (Fasoula and Fasoula 1997). This acquired dissimilarity is environmental/external in nature and could be as a result of differences in cutting quality, micro-site, planting technique, etc. Any ramet with a head start, as a result of some external factor, is not likely to be surpassed by another ramet of the same clone because both have the same growth potential and resource requirement. This initial difference is likely to be increased after canopy closure as a result of overshadowing, especially if the clone involved is a strong competitor. Donald (1968) *as cited by Fasoula and Fasoula (1997)* states that in the ideal crop environment, individual plants of the mono-genotypic community should be weak competitors in order to encroach to a minimum degree on the resources available for their like neighbours. Brouard and John (2000) state that it is possible for different clones to respond differently to different planting densities, and therefore clonal selection and the identification of optimal cultural conditions need to be carried out together. “The highest yielding clone in a clonal block planting at a given spacing may not outperform other clones if the spacing is changed”.

2.1.3. Under compensation vs. over compensation.

Under compensation is where yield gains of some plants in a stand fail to compensate for yield losses of other plants as a result of unequal sharing of resources. Therefore yield per unit area is reduced. This occurs in both the crop and competition environments (Fasoula and Fasoula 1997).

Over compensation is where the unequal use of density limited growth resources results in yield gains from competition (increased growth of dominant trees), which exceed the yield losses (reduced growth of suppressed trees), with the net result being an increased production per unit area (Fasoula and Fasoula 1997). This is however only likely if the reason for size differences/unequal sharing of resources is genetic, and the dominant

trees have some inherent ability to more efficiently convert available resources into biomass. This can only occur in the competition environment (different genotypes) (Fasoula and Fasoula 1997).

2.1.4. Stages of competition in a stand.

Neighbour influences (competition) on a subject plant span from first “sign of presence”, to mortality (Von Euler *et al*. 1992). In a fertilizer x irrigation trial in *Eucalyptus* Tomé *et al*. (1994) noticed two distinct stages in stand development: initially the coefficient of variation (CV%), for size, was high followed by a steep decrease and a period of stability or slight increase in CV%. Bouvet (1997), Von Euler *et al*. (1992), and Little (1999) noticed a similar trend. Little (1999) showed that the reduction in CV% was as a result of a reduction in the differences between the growth rates of smaller and bigger trees just prior to the reduction in CV%. Tomé *et al*. (1994) suggest that the initial high size variability may be a consequence of different responses of seedlings to transplanting and that the decrease in variability there after may simply correspond to the recovery of the more affected seedlings. They also found that initially small trees were not suppressed and that they had higher relative growth rates (RGR) than larger trees (RGR is explained at a later stage). Brand and Magnussen (1988) showed that at low density, smaller trees generally show greater vigour. They suggested that this could be as a result of these smaller trees being more efficient due to lower maintenance respiration levels per unit of foliage. They found that as density increased, being smaller became a handicap in making use of a resource such as light thereby reducing vigour.

By consolidating the findings of all the above authors stand development can be described in terms of three stages as follows:

(1) Free exponential growth; which is characterized by large size variability due to genetic differences, micro-site differences, seedling size and/or quality differences and differences in response to transplanting. Trees are not yet in competition with each other.

(2) Catch-up stage; in which size variability is markedly reduced. This may be a result of larger seedlings becoming less efficient in terms of maintenance respiration required for supporting foliage, thereby inducing a slowed relative growth rate (RGR). This leads to smaller trees catching up and therefore lower size variability.

(3) Trees come into competition with each other thereby reducing overall relative growth rates. A gradual increase in size variability due to intra-specific competition occurs. Poorer competitors become suppressed thereby increasing size variability in the stand. Suppressed trees usually die, therefore the increased size variability is not as large as would be expected.

2.1.5. Competition symmetry and directionality

Brand and Magnussen (1987) describe the process of competition in terms of symmetry and directionality (one- or two-sidedness). Symmetry in competition

implies that the resource availability falls below the sum requirement of a population and all individuals share the limited quantity in relation to their size. Any degree of deviation from perfect sharing relative to its size is asymmetry. Competition is symmetric if a scarce resource is utilised by competing neighbours in proportion to their size, but asymmetric if, say, the larger neighbours obtain disproportionately more resource (West *et al*. 1989 as cited by Von Euler *et al*. 1992). Two-sided competition implies that with a limited resource, all plants in a population are affected to some degree, and even small plants affect the growth of larger neighbours. One-sided competition- implies that larger plants affect the growth of smaller plants and not the other way around. Therefore one-sided competition is always asymmetrical, whereas two-sided competition can be either symmetrical or asymmetrical. Asymmetry describes the inequality of resource sharing, while two-sidedness describes the magnitude of “downward” (large vs. small) and “upward” (small vs. large) competition (Brand and Magnussen 1987).

2.1.6. Resource depletion vs. resource pre-emption.

"Intra-specific competition within even-aged, mono-specific plant populations has been conceptualised as a continuum ranging from a resource depletion process, to a resource pre-emption process" (e.g., Koyama and Kira 1956; Ford 1975; Mohler *et al*. 1978; West and Borough 1983; Cannell *et al*. 1984; Brand and Magnussen 1988; Thomas and Weiner 1989; Newton 1990; Schwinning and Fox 1995; Weiner *et al*. 1997) as cited by (Newton and Jolliffe 1998a and 1998b). The processes of resource depletion and pre-emption have differential effects on the distribution of relative growth rates and resultant size hierarchy developmental patterns within density-stressed plant populations (Weiner 1990 *as cited by* Newton and Jolliffe 1998a).

The resource depletion process is characterized by a symmetrical relationship in which competitors share the limited resources in direct proportion to their relative sizes (Weiner 1990 *as cited by* Newton and Jolliffe 1998a). It is also thought to involve competition for below ground resources, in which competitors deplete the available soil resources in direct proportion to their relative sizes (e.g., Weiner, 1985; Lieffers and Titus 1989; Weiner *et al*. 1997) *as cited by* (Newton and Jolliffe 1998a, 1998b). The resource depletion process has been characterized by equivalent declines in relative growth rates across size classes (Weiner 1990; Hara 1992 *as cited by* Newton and Jolliffe 1998a).

Conversely, the resource pre-emption process is characterized by an asymmetrical relationship in which competitors share the limited resources disproportionately in relation to their relative sizes (i.e., larger-sized competitors acquire a greater portion of the limited resource than smaller sized competitors on a per unit size) (Weiner 1990 *as cited by* Newton and Jolliffe 1998a, 1998b). It is thought to involve competition for aboveground resources in which larger-sized competitors passively prevent solar resources from reaching smaller-sized competitors (e.g., Weiner 1986; Peterson *et al*. 1990) *as cited by* (Newton and Jolliffe 1998a, 1998b). The resource pre-emption process has been characterized by inverse size dependant declines in relative growth rates across size-classes resulting in increased relative

growth rate variation and hence increased size-inequality at increasing levels of density stress (Weiner 1990; Hara 1992 *as cited by* Newton and Jolliffe 1998a). Other authors advance the hypothesis that competition for light is asymmetric whereas competition for nutrients is two-sided, but not necessarily symmetrical, namely (Ford and Diggle, 1981; Weiner, 1986) as cited by Tomé *et al*. (1994).

Findings supporting the hypothesis that resource pre-emption is the dominant competition process in even aged monocultures include: Sitka spruce (Ford 1975; Cannell *et al*. 1984), balsam fir (Mohler *et al*. 1978), radiata pine (West and Borough 1983), lodgepole pine (Cannell *et al*. 1984), red pine (Brand and Magnussen 1988), jack pine (Magnussen 1989) and pitch pine (Thomas and Weiner 1989) *as cited by* Newton and Jolliffe 1998a.

Conversely, support for the hypothesis that resource depletion is the dominant competition process has been usually limited to the establishment phase of population development and or to populations at relatively low levels of density stress (e.g. Newton 1990; Newton and Jolliffe 1993; Stoll *et al*.1994) *as cited by* Newton and Jolliffe 1998a.

The occurrence of a resource-depletion process during the early stages of stand development was noticed by Newton and Jolliffe (1990 and 1993). It is difficult, if not impossible, to define an exact zone of influence of individual trees that includes all competitors and sources of competition for scarce resources. For example, Stiell (1970 as cited by Biging and Dobbertin 1995) found that aboveground competition is concentrated within the area occupied by individual crowns, but that root competition is diffuse and is unpredictable for a given tree (Biging and Dobbertin 1995).

Historically, the main indicator used to distinguish between resource depletion and resource pre-emption has been stem growth responses at (1) individual tree, (2) size-class or (3) stand-level. (e.g. Ford, 1975; Cannell *et.al*., 1984; Stoll *et.al.*, 1994; Newton and Jolliffe, 1998a; Brand and Magnussen, 1988; Knox *et al*., 1989; Newton, 1990) *as cited by* Newton and Jolliffe 1998b.

2.1.7. Modular responses to competition

As a stand develops and a few plants become large, the smaller plants appear to "adjust" to their new environment and become morphologically different. Forest trees are modular organisms and may exhibit adaptive, plastic responses in phenotype to intra-specific competition by changing their internal allocation of resources (Harper, 1977; Sultan, 1987 *as cited by* Newton and Jolliffe 1998b). Therefore competition may affect the growth characteristics of different modular components. Plasticity that individuals exhibit as competition intensifies may reflect an ecological strategy that may have evolved in response to restricted resource availability. Evolution of the size dependence of growth of modular components, and the investigation of patterns of dry matter partitioning, may provide a more definitive assessment of competition processes and strategies. These plastic responses were used by Newton and Jolliffe (1998b) in an attempt to identify the dominant

competition process (resource depletion or resource pre-emption) present in density stressed black spruce stands.

Newton and Jolliffe (1998b) found branch production was the component most affected by intra-specific competition. They also found that directional specific relationships in which competition from larger sized competitors resulted in reduced commitment to branch production including branch retention in smaller trees. These results were in accordance with other findings of reduced branch growth and increased abscission as a result of shade induced reductions in light intensity (e.g. Duff & Nolan, 1961(a) and 1961(b); Millington and Chaney, 1973; Cochrane and Ford, 1978; Makinen, 1996 as cited by Newton and Jolliffe 1998b). Competition by resource pre-emption is considered to be an aboveground process in which larger-sized competitors capture a disproportionately large share of the light resource at the expense of smaller sized individuals (Peterson *et.al*., 1990 as cited by Newton and Jolliffe 1998b). Therefore growth indices related to light capture and usage should be well suited to detect the occurrence of competition by resource pre-emption. Increase in SLA (specific leaf area ($cm^2.g^{-1}$)) as competition increased from above would act to enhance the light harvesting capability of suppressed individuals. Newton and Jolliffe (1998b) found; (1) Suppressed trees display a greater area of foliage per given branch mass due to an increased specific leaf area; (2) Foliage production was preferentially maintained over branch and stem production as competition increased; (3) Responses of nutrient concentrations to increasing local competition were non-directional, suggesting that competition for nutrients was not the dominant interaction among competing trees.

2.1.8. Process of Self-Thinning.

In stands at or near carrying capacity, increased growth by dominant individuals results in overtopping, suppression and eventually mortality of smaller neighbours (Brand and Magnussen, 1988). As dominants continue to compete for the fixed amount of space and resources, there is a continual self-thinning of trees in intermediate or suppressed crown positions (West and Borough, 1983 as cited by Brand an Magnussen, 1988).

Newton and Jolliffe (1998b) explain how mortality occurs in suppressed trees. As branch production approaches a minimum in terms of mechanical support and foliar adjustments approach a maximum in terms of SLA, additional declines in light resources due to increasing dominance of larger sized-competitors may result in reduced rates of photosynthesis. These reduced rates of photosynthesis combined with increased non-photosynthetic area may cause a negative carbon balance leading to mortality. This inference is similar to that proposed for the natural senescence process for forest tree species proposed by Watkinson (1992 as cited by Newton and Jolliffe, 1998b).

Self-thinning occurs regularly, bounded by some maximum carrying capacity of leaf area or biomass at a given density (Yoda *et al.* 1963, Weller 1987 as cited by Brand and Magnussen, 1988).

2.1.8.1. Yoda's Self-thinning Law

The self-thinning rule was first proposed by Tadaki and Shidei (1959 as cited by Zeide 1985), in their study of the self-thinning of *Cryptomeria japonica*, and further investigated by Yoda *et al*. (1963 as cited by Zeide 1985). The self-thinning rule was introduced to western literature by White and Harper (1970 as cited by Zeide 1985), who used numerous examples from forestry.

Considered one of the most robust and widely applicable theoretical models for describing intra-specific density-dependant regulation in plant populations (Pitelka, 1984 as cited by Zeide 1985), and it is the first basic law demonstrated for ecology (Harper, 1977 as cited by MacIntosh, 1980 and Zeide,1985). The self-thinning rule uses an average tree or, more generally, plant weight or volume (*v*), rather than the diameter, as an indicator of plant size:

$\ln v = c - (b_1 \ln (N))$ (v is the average volume per tree and N the stems per unit area) [Equation 1]

where: *c and b_1 are coefficients*
v = average volume per tree
N = the number of stems per unit area

This equation forms only the background for the self-thinning rule. The rule itself is a statement that coefficient b_1 is a constant equal to 3/2 for all species and locations (Zeide 1985).

Zeide (1985) and Bi *et al*. (2000) converted this equation to use stand volume/mass per hectare in place of average tree volume or mass as follows.

Adding *ln N* to both sides of [equation 1] results in:

$\ln V = \ln (vN)$

$\ln V = c-(b \ln (N))$ [Equation 2]

where: *V = v x N (the volume of all trees per unit area)*
$b = b_1-1=0.5$

White and Harper (1970 as cited by Zeide 1985) found that all lines representing self-thinning of tree species have slopes (b_1 in equation 1) between 1.72 and 1.82, considerably steeper than expected. Breedenkamp (1988) found the slope b (equation 2) to be between 0.91 and 0.80 with an average of 0.87, in *Eucalyptus grandis* seedlings in Zululand as opposed to 0.5 stated in the theory. He also found the slope to be strongly affected by age. The rule is applicable only at the intermediate stage of stand development in which the canopy is closed, when the tolerance remains constant (Zeide, 1985). The rule has been applied to a wide variety of species and densities, and received favourable comments in forestry literature (Drew and Flewelling, 1977, 1979; Binkley, 1984; Long, 1985; *as cited by* Zeide

1985). From an investigation of some 80 species, White (1980 as cited by Zeide 1985) confirmed the constancy of the slope (b_1) and concluded “the empirical generality of the rule in its original formulation (Yoda *et al*. 1963) is now beyond question”. According to Zeide (1985) b is a variable rather than a constant (the coefficient changes systematically with species and site). Zeide (1985) states that the variability of b may be its greatest asset. "Instead of constancy, it presents a valuable indicator of the properties of tree species and stands". The coefficient b usually exceeds the expected ½ (3/2 for b_1). Along with these findings Zeide (1985) states that “ It is contrary to forestry knowledge to believe that self-thinning of all stands in the world can be expressed by the same constant”.

A large number of authors can be quoted that either accept or reject the consistency of the slope. According to Bi *et al*. (2000) much of the debate has centred on the empirical validation of the self-thinning rule, where the lack of objectivity has become the stumbling block. The common methods of estimating the boundary line have been to choose data points that exhibit density-dependent mortality and lie close to an arbitrarily visualised upper boundary before the line is estimated, and to subjectively eliminate data points from populations that are believed to be undergoing density-dependent mortality. The selected points are then used to estimate the line through principal components analysis or reduced major axis regression. Due to the subjectivity involved, the same data set can be analysed by some to provide evidence for rejection and re-analysed by others to reach different conclusions (Bi *et al*.2000). Bi *et al*. (2000) demonstrated how stochastic frontier production functions developed in econometrics for the analysis of maximum potential output could be used to estimate the self-thinning boundary line objectively, without data selection, using data from even-aged *Pinus radiata* stands. They concluded that the slope they calculated using this method was not significantly different to -0.5 (value for b in equation 2) at the 95% confidence level.

There are some very important applications of this self-thinning rule, whether the slope, b or b1, is constant or not. The self-thinning line can be used to determine when thinning should be carried out, and the intensity of those thinnings operations, with a particular piece-size in mind for saw-timber crops (e.g. Archibald and Bowling 1995). It can also be used to estimate and understand the impacts of initial planting density on different species and sites for pulp-timber crops.

2.1.9. Self-Tolerance.

Zeide (1985) defines tolerance as “the ability of an organism of biological process to subsist under a given set of environmental conditions”. Tolerance depends on many factors (Wenger, 1984 as cited by Zeide 1985), both external (temperature, latitude, altitude, soil moisture and fertility) and internal (genotype and age). Tolerance is characterised by numerous criteria, which rarely provide a unanimous rating of species (Ziede 1985). Many criteria for estimating the tolerance of species have been proposed by various authors. One of the tolerance criteria mentioned most often is the rate of self-thinning (Zeide 1985). The concept of tolerance is clear and useful when it is restricted

to a subset of intrinsically related properties, but becomes ambiguous and misleading when it goes beyond this subset.

Zeide (1985) proposed that the intra-specific competitive ability of trees be referred to as "self-tolerance", a quality independent of "tolerance". The relative rate of volume growth with respect to the decrease of the number of trees (self-thinning rate) captures both processes involved in the definition of self-tolerance (growth and mortality) and can be used as its measure. Zeide (1985) demonstrated that the slope *b* (equation 2) is equivalent to self-tolerance (S) and that the larger the value, the more self-tolerant is the stand/species/genotype. Therefore the same proportional increase in volume is accompanied by lesser mortality in more self-tolerant species. Alternatively, given the same mortality, a greater proportion of volume is accumulated in stands of greater self-tolerance. Zeide (1985) also found that self-tolerance tended to increase with an increase in site quality.

2.2. Quantifying competition

2.2.1. Measures of vigour

Vigour of an individual tree, size-class or stand can be used to describe both the direction and intensity of competition.
Vigour can be quantified using a number of measures. The advantages and shortcomings of some of these measures are presented below:

Growth (G) = x(t) (measures size) [Equation 3]

Size alone gives no indication of vigour. Therefore it cannot be used to measure competition effects.

Growth rate (GR) = $\left(\frac{d(x)}{d(t)}\right)$ (measures size increment) [Equation 4]

Growth rate does measure vigour. It may however be misleading when trying to detect competition effects. Growth in trees is largely determined by current size in even-aged populations, and slight systematic changes in size increment, attributable to differences in competition, are not readily apparent (Brand and Magnussen, 1988). This measure is acceptable for stand level comparisons, but not for comparing individual trees or size classes within a population.

Relative Growth Rate (RGR) = $\left(\frac{d(x)}{d(t)}\right) x \frac{1}{(x)}$

(measures rate of change in size per unit size) [Equation 5]

This measure acts to remove the influence of size on growth, allowing direct comparison of the vigour of large and small plants. While effective for annual or short-lived perennial plants, RGR looses the feature of size independence when applied to long-lived plants such as trees. Trees accumulate very large amounts of non-reproductive stem wood and other tissues, which become a much greater determinant of relative growth rate than the differences in

annual increment, or its changes from year to year (Brand and Magnussen, 1988).

$$\text{Relative Production Rate (RPR)} = \frac{\left(\frac{d(x)^2}{d(t)^2}\right)}{\frac{(d(x))}{(d(t))}}$$

(measures rate of change in size increment per unit increment) [Equation 6]

Brand and Magnussen (1988) proposed the use of RPR. They state that it measures whether the annual growth is increasing, constant or diminishing, and is a more reasonable measure of growth vigour in trees.

Newton and Jolliffe (1998b) presented the RPR equation as follows:

$$RPR = \frac{d\left[d(x)/d(t)\right] \big/ d(t)}{d(x) \big/ d(t)} \qquad \text{[Equation 7]}$$

Various size variables can be used in the above measures, namely: diameter at breast height (DBH), basal area, tree height, tree weight and tree volume. Newton and Jolliffe (1998b) used foliage mass, branch mass and stem mass individually, as size variables in the RPR measure. There are advantages and disadvantages associated with most size variables used. DBH is quick and cheap to measure, with very little error associated. Tree height takes longer and is more expensive to measure. There is a significant degree of error associated with tree height measurement. Bruce (1975 as cited by Williams and Schreuder 2000) point out that the accuracy in height measurement is limited by an interaction of instrument, observer and stand conditions. Williams *et al*. (1994 as cited by Williams and Schreuder 2000) suggest that error in height measurement increases proportionally with tree height and that measurements on hardwoods are generally less accurate than measurements on softwood trees. Tree volume can be directly measured with destructive sampling, which is expensive, and time consuming. Indirect measurement of volume entails the use of DBH and tree height in an equation. This increases the potential source of error greatly (error associated with height measurements plus error associated with equation). Stem mass is difficult and expensive to measure directly as it requires destructive harvesting. Stem mass can be calculated with the use of allometric equations. This however increases the potential error (error associated with the allometric equation). From Brand and Magnussen (1988) it is clear that it is not only the error associated with measurement of the size variable that is a problem. They state that, different findings regarding competition in the literature may be as a result of differences in the choice of size variable. Trees with different initial diameters may produce the same diameter growth in a year but will not produce the same increase in stem area. For this reason basal area is a better size variable than diameter. In conditions of intense competition, trees

may show no diameter growth on the lower stem (where diameter measurements are taken), despite growth continuing on the upper stem (Farrar 1961 as cited by Brand and Magnussen 1988). For this reason Brand and Magnussen (1988) recommend the use of tree volume as a measure of tree size as it integrates growth over the entire stem. It is therefore clear that finance, time and error must be weighed up in the selection of size variables used when trying to measure competition effects.

When comparing stands or treatments of a spacing trial for competitive effects a dilemma arises. Do we compare treatments at equal age, or do we compare treatments at equal mean tree size. Brand and Magnussen (1988) argue that by comparing treatments at equal mean tree sizes, the common problem of comparison at both different mean size and different density is removed. They do however admit that there may be a confounding effect when comparing stands at different ages. This would only be true if the biological age of trees affects their growth rate. This is however unlikely with the short rotations used in South Africa.

Comparing treatments with equal mean size poses another problem. The growth trajectory of each tree in each treatment will have to be calculated by means of regression. Each tree would then need to be grown forward or backward until the desired mean tree volume is obtained. The error involved could prove to be very large.

2.2.2. Level at which competition is measured

Competition effects can be observed at a number of levels, from the responses of individual trees to the effects of competition on the dynamics of the stand (Tomé *et al*. 1994). Four levels of detail are usually considered when measuring competition effects. (i) Effect of competition on the modular components of the individual tree. (ii) Effect of competition on overall growth of the individual tree. (iii) Effect of competition on a particular size class within a stand. (iv) Effect of competition on the entire stand.

2.2.2.1. Individual tree responses to competition

Individual trees in a stand react to competition in a number of ways. These reactions can be in the form of one or all of the following: (a) changes in resource allocation, (b) changes in physical proportions of the various modular components, or (c) changes in vigour.

2.2.2.1.1. Changes in morphology of modular components of the tree

Measuring the size and or dimensions and or nutrient contents of various portions of the tree may give an indication of some of the competition processes at work.

Some measures that can be used include: leaf area, leaf area index (LAI)($m^2.m^{-2}$), SLA ($cm^2.gm^{-1}$), branch mass, nutrient concentration in various portions. These measures are useless unless the interaction between them and other factors are quantified. An example of this would be comparing nutrient content in the leaves of dominant trees with that in suppressed trees (tree-size by nutrient concentration interaction), as done by Newton and

Jolliffe (1998b). Newton and Jolliffe (1998b) also used the interaction between trees size/competitor status and SLA to see how suppressed trees adjust to reduced light. Measuring these variables is expensive and time consuming, therefore it can only be done on a small scale in order to develop allometric equations. These allometric equations enable the use of surrogate, easier to measure variables.

2.2.2.2. Size-class response to competition

Size-class responses to competition involve measures of vigour. Measures of vigour by size class were used by Brand and Magnussen (1988) to determine competition symmetry, competition direction and whether competition was one-sided or two-sided.

2.2.2.3. Stand level responses to competition

Stand level responses to competition involve measures of the size distribution, measures of size variability and measures of vigour.

2.2.2.3.1. Co-efficient of variation or Gini Co-efficient.

The Gini-coefficient is a measure of inequality in size (Weiner and Thomas 1986 *as cited by Brand and Magnussen 1988*) and proves very similar to the coefficient of variation (CV%). The coefficient of variation or Gini-coefficeint can be applied to a measure of size, e.g. DBH, basal area, height or volume. Brand and Magnussen (1988) and Bouvet (1997) used individual tree volume as the measure of size. Little (1999) used DBH. Tomé *et al*. (1994) used individual tree basal area. Von Euler *et al*. (1992) used both height and individual tree basal girth.

2.2.2.3.2. Skewness

Skewness indicates a departure from normality in a frequency distribution, with the median size being greater than the mean in the case of negative skewness (skewed to the right) and vice versa in the case of positive skewness (skewed to the left) (Brand and Magnussen 1988). With an increase in competition/planting density the distribution skewness moves from a negative to a positive. A negative skewness means that there are more big trees and fewer small trees, whereas a positive skewness indicates the presence of more small trees and fewer larger ones.

2.2.2.3.3. Stand vigour

Comparisons in terms of whole stand vigour can be made between different stands or treatments of a trial. This can be done at equal age or equal mean tree size.

2.3. Aim

- To describe and compare competition processes in even-aged stands of the *Eucalyptus* genotypes tested.

2.3.1. Objectives

- To describe and compare the competition processes at work in the genotypes tested.
- To test the applicability of competition measures found in the literature, to selected *Eucalypt* plantations grown in South Africa.
- To understand the effect of the interaction between competition process and genotype, resulting from initial planting density manipulation, on stand productivity.

2.3.1.1. Key questions

- Is there a difference in the degree of self-thinning between the clone and the seedling, and what is the magnitude of this difference if it is present?
- Are smaller competitors reducing the growth rate of larger competitors? Can this be quantified, and how does this differ between genotype?
- Can a combination of the self-thinning rate and some measure of intensity of upward competition, be used to understand the effect of planting density (therefore competition) on plantation productivity.

2.4. Hypotheses

a) Increased stand density results in increased competition between individuals within the stand.
b) Larger trees use disproportionately more resources than smaller ones and therefore competition is asymmetrical.
c) When trees in a stand are competing for resources, smaller competitors take up some of the resources required by the larger ones, thereby slowing their growth, therefore competition is two-sided.
d) Suppressed trees in the clonal treatments reduce the growth of larger competitors to a greater extent than do the suppressed trees in the seedling treatments.
e) The rate of self-thinning in the seedling is higher than in the clone.
f) A combination of lower self-thinning rate and greater proportional reduction in growth of larger competitors as a result of competition from smaller competitors, will result in the clonal treatments being more detrimentally affected by between-tree competition than the seedlings.

2.4.1. Hypothesis 1:

“Increased stand density results in increased competition between individuals within the stand.”

By definition, “competition is the interaction between individuals for a shared resource which results in a reduction in survivorship, growth and or reproduction” (Begon *et al*. 1990). If it could be proved that increased planting density results in a reduction in growth, and reduced growth is a result of

competition (as per definition), then it could be argued that increased planting density results in increased competition between individuals. By comparing plots with equal mean tree size and the only difference between them being planting density, if mean vigour was found to be lower in plots with higher stand densities it would have to be accepted that increased planting density results in reduced growth and therefore increased competition between individuals.

Therefore if at equal mean tree size, treatments at a higher planting density have less vigour (RPR and RGR) than those at a lower planting density, then the hypothesis should be accepted.

This was tested as follows:

a) Mean tree size was modelled through time on a per plot basis using regression techniques.
b) The growth of each tree was modelled through time using regression techniques.
c) Using the individual plot regression equations, the age at which mean tree size was equal to some pre-defined value was calculated. These ages were then entered into the individual tree models.
d) The mean RPR and RGR per plot was then calculated, and compared across the various planting densities being tested, using analysis of variance.

2.4.2. Hypothesis 2:

“Larger (dominant trees) use disproportionately more resources than smaller trees and therefore competition is asymmetrical.”

More vigorous growth is as a result of increased or more efficient resource usage. Therefore if it can be proved that larger trees grow more vigorously than smaller ones, the hypothesis can be accepted.

This was tested as follows:

a) Trees within each plot were placed into size-classes. Mean tree vigour within each size class was analysed when all plots in the trial had the same mean tree size.
b) If larger size classes had greater vigour than the rest then the hypothesis was accepted.

2.4.3. Hypothesis 3:

“When trees in a stand are competing for resources, smaller competitors take up some of the resources required by the larger ones, thereby slowing their growth, therefore competition is two sided.”

Compare the average vigour of dominant trees within plots with many smaller trees (higher planting density), with the average vigour of dominant trees of

the same size, within plots with fewer smaller trees (lower planting density). If it is found that those dominant trees within plots with fewer smaller trees (lower planting density) are growing more vigorously, the hypothesis can be accepted. The only difference between the two is the presence of different numbers of smaller trees. If there are more small trees present, and growth is slower, then it must be assumed that this slower growth is as a result of the presence of these smaller trees, which are using resources required by the bigger trees.

This was tested as follows:

a) Isolate a pre-determined number of the largest trees per plot. Calculate the average size per plot of these dominant trees at each measurement event.
b) Use regression techniques to model the progression of this average size of dominants per plot with time.
c) Use this model to calculate the age at which the average size of dominants per plot is equal to some pre-determined size. Insert this age into the individual tree models, so that the vigour of each dominant tree can be calculated.
d) Calculate the average RPR and RGR of these dominant trees on a per plot basis. Compare the average RGR and RPR of dominant trees within different planting densities.

2.4.4. Hypothesis 4:

“Suppressed trees in the clonal plots reduce the growth of the larger competitors (dominants) to a greater extent than do the suppressed trees in the seedling plots.”

This was tested as follows:

a) Hypothesis 3 would need to be accepted.
b) Exactly the same procedure was followed as in hypothesis 3, except the vigour (RPR and RGR) of the dominant trees in the seedling high planting density plots was compared with the vigour of the dominant trees in the clonal high planting density plots.
c) If the dominants in the seedling high planting density plots had statistically significantly greater (vigour) than the dominant trees in the clonal high planting density plots, the hypothesis could be accepted.

2.4.5. Hypothesis 5:

The rate of self-thinning in the seedling is greater than in the clone. This was tested by comparing the slopes of the lines defining the surviving stems.ha^{-1} vs. time relationship for the various treatments. The relationship between surviving stems.ha^{-1} and average tree volume was also analysed.

2.4.6. Hypothesis 6:

A combination of lower self-thinning rate and greater proportional reduction in growth of larger competitors, as a result of competition from smaller competitors, will result in the clonal treatments being more adversely affected by between-tree competition than the seedlings.

Hypotheses 4 and 5 needed to be accepted. If hypothesis 5 was accepted, it would have had to be proved that the lower self thinning rate of the clone resulted in reduced overall production.

Chapter 3. Materials and methods

3.1. Trial description

The simplest method of evaluating competition effects in forest stands is through the use of spacing trials. Spacing trials create stands/plots in which all silvicultural and climatic variables are constant. Changes in vigour and distribution of this vigour within and between treatments can then be attributed to competition alone.

This trial was planted on the 5th of December 1996. It was blanked (dead plants replaced) on the 19th of December 1996.

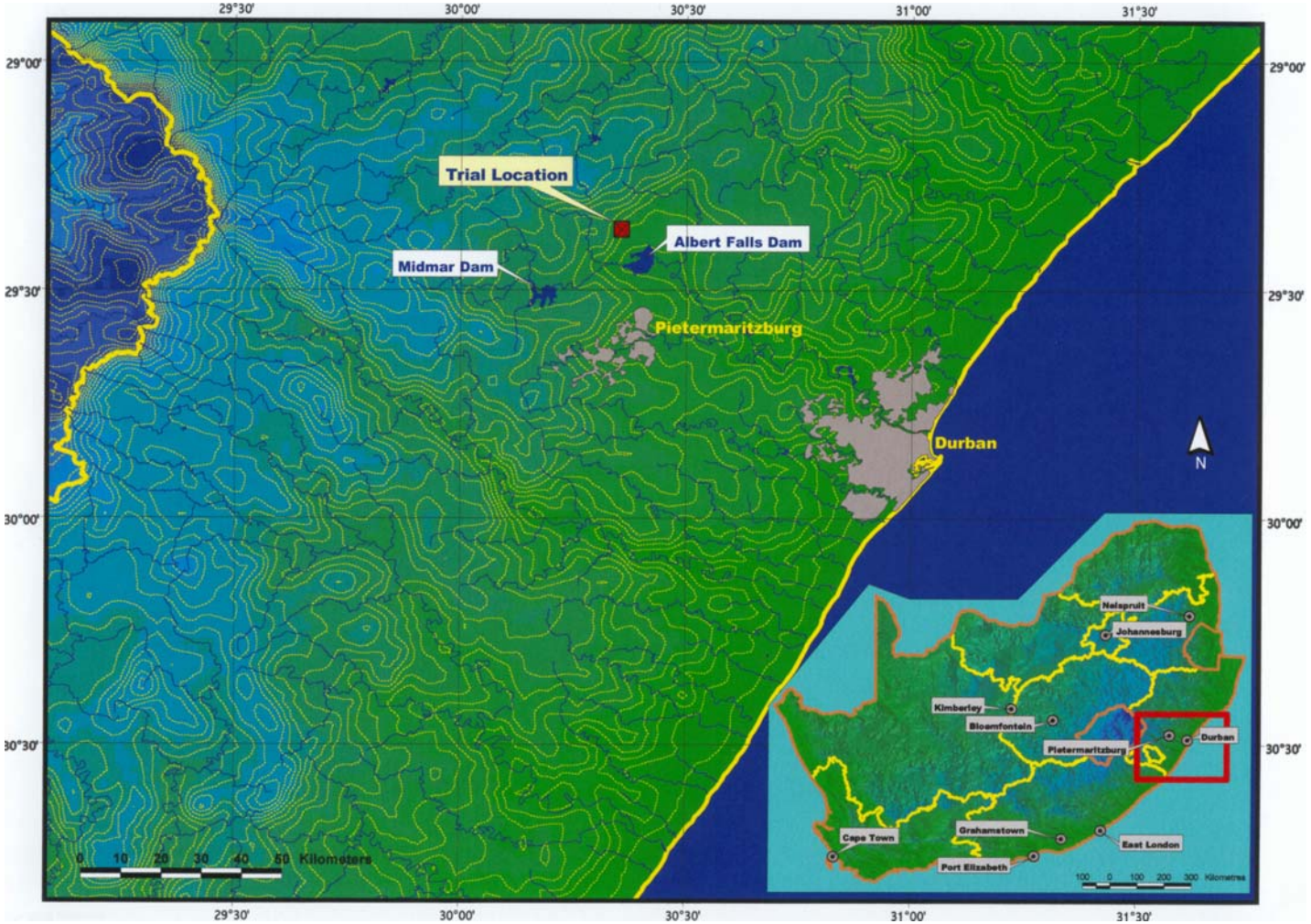
3.1.1. Trial location

The trial is located on Sappi's Clan plantation in the KwaZulu-Natal Midlands at latitude -29.37 South and longitude +30.35 East. It is situated 28 km North of Pietermaritzburg, 7 km and 84 km North West of the Albert Falls dam and Durban respectively (see map 1).

3.1.2. Site description

The trial is located in the Summer-rainfall region of South Africa. The site chosen has an estimated mean annual precipitation (MAP) of 1143 mm. It is situated at 900 metres above sea level (m a.s.l.) with a mean annual temperature (MAT) of 17.6 ^{o}C (Pallett and Mitchell, 1993). The terrain is flat with deep apedal red soils. The previous crop was *Pinus taeda*. Land preparation involved pitting into broadcast slash.

Map 1: Location of the trial



3.1.3. Trial design

The initial aim of the trial was to test the effect of planting density and genotype on a highly productive site with the aim of reducing rotation length.

A split-plot design with six replications was used, with planting density being the whole-plot factor and genotype being the sub-plot factor. The sub-plots were 15m x 15m in extent. Five planting densities were evaluated. The five treatments were planted with 3.0m spacing between rows (resulting in five rows per plot), and within-row spacing of either 0.5m, 1.0m, 1.5m, 2.1m or 3.0m; resulting in planting densities of 6667 stems.ha^{-1}, 3333 stems.ha^{-1}, 2222 stems.ha^{-1}, 1587 stems.ha^{-1} and 1111 stems.ha^{-1} respectively. The reason for maintaining three metres between rows was to simulate an allowance for the movement of machinery within the stand. The genotypes used were a *Eucalyptus grandis* seedling (seedstock no P4969) and a *Eucalyptus grandis x urophylla* hybrid clone (W1022).

						1587spha Clone	1111spha Seedling	2222spha Seedling	3333spha Seedling	6667spha Clone	Rep 1
						1587spha Seedling	1111spha Clone	2222spha Clone	3333spha Clone	6667spha Seedling	
						6667spha Clone	2222spha Clone	1587spha Clone	1111spha Seedling	3333spha Seedling	Rep 2
Rep 5	2222spha Seedling	1111spha Seedling	1587spha Clone	3333spha Seedling	6667spha Seedling	6667spha Seedling	2222spha Seedling	1587spha Seedling	1111spha Clone	3333spha Clone	
	2222spha Clone	1111spha Clone	1587spha Seedling	3333spha Clone	6667spha Clone	3333spha Clone	2222spha Seedling	1587spha Seedling	6667spha Seedling	1111spha Clone	Rep 3
Rep 6	1587spha Seedling	6667spha Clone	1111spha Clone	3333spha Seedling	2222spha Seedling	3333spha Seedling	2222spha Clone	1587spha Clone	6667spha Clone	1111spha Seedling	
	1587spha Clone	6667spha Seedling	1111spha Seedling	3333spha Clone	2222spha Clone	1111spha Clone	6667spha Seedling	1587spha Clone	2222spha Seedling	3333spha Seedling	Rep 4
						1111spha Seedling	6667spha Clone	1587spha Seedling	2222spha Clone	3333spha Clone	

Figure 1: Trial Design

3.2. Sampling and measurement strategy

3.2.1. Mensurational data acquisition strategy

The trial has been intensively measured, with collar-diameter (using a diameter tape) and height measurements (using a height rod) being taken at 2.5 months, 4.8 months and 9.6 months respectively. Diameter at breast height (DBH) and height (using a vertex hypsometer) were measured at 1.0 year, 1.4 years, 1.9 years, 2.5 years, 3.4 years, 4.4 years, 5 years and 5.5 years respectively.

Only the inner three rows were measured on each occasion, thereby leaving two buffer rows of 3m each between measured plots. All the measured plots are of equal area (9m x 9m) with the exception of the 1587 stems.ha^{-1} treatment with a plot area of 9m x 10.5m (this is because a 2.1 m spacing cannot fit into a 9m space without a remainder), resulting in a different number of trees being measured for each planting density treatment. DBH measurements of 54, 27, 18, 15 and 9 trees per plot were taken. Trees in the middle row were measured for height in the 6667 stems.ha^{-1}, 3333 stems.ha^{-1},

2222 stems.ha^{-1} treatments, and the heights of all measured trees in the 1587 stems.ha^{-1} and 1111 stems.ha^{-1} treatments. Therefore 18, 9, 6, 15 and 9 height measurements per plot were made for the 6667 stems.ha^{-1}, 3333 stems.ha^{-1}, 2222 stems.ha^{-1}, 1587 stems.ha^{-1} and 1111 stems.ha^{-1} treatments respectively. The number of heights per plot to be measured was calculated so as to have at least 30 DBH/height pairs from which the height of unmeasured trees could be modelled.

3.2.2. Destructive sampling strategy

A destructive sampling exercise was carried out in rep 4 in June 1999 and in rep 6 in June 2002. The strategy used is explained below.

3.2.2.1. Sample selection

At each sampling event, one replicate, with four trees per plot, was selected for biomass determination. In each plot one tree was selected at random from the smallest DBH group comprising one third of plot basal area (BA), one from the largest trees comprising one third of the plot BA and two from the remaining mid-size trees (figure 2). Trees with broken tops, forked stems or any other abnormalities were excluded for sampling purposes.

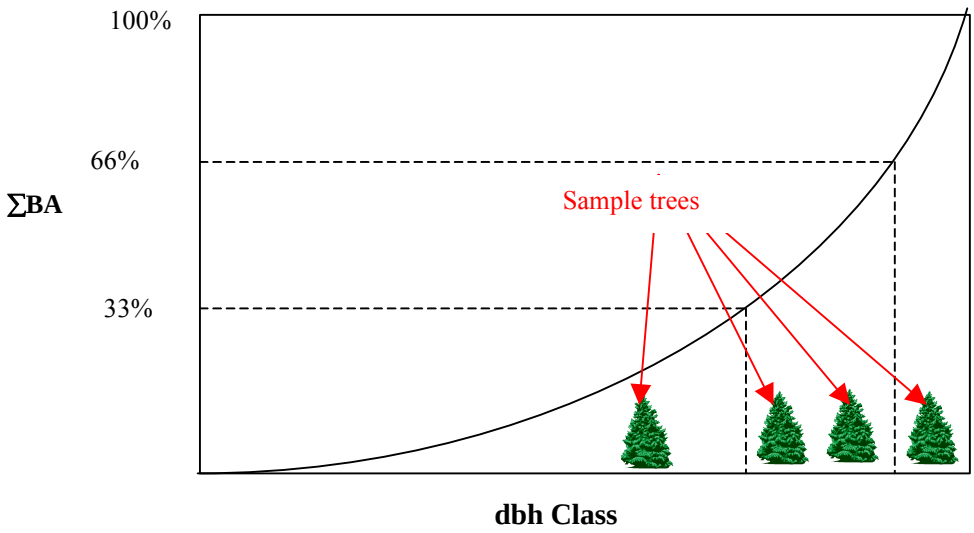


Figure 2: Sampling method for destructive sampling of fourth replicate.

3.2.2.2. Sampling methodology.

3.2.2.2.1. In field

A large sheet of plastic was laid out on the plantation floor below the pre-selected trees. All dead branches still attached to the tree, within reach of a person on a ladder, were removed prior to felling the tree. The tree was then felled onto the sheet of plastic. All remaining dead branches were then removed. All the dead branches were weighed in field. A sub-sample was then placed in a sealed plastic bag, labelled and stored in a cooler box (to preserve the moisture in the sample). All the leaves were picked from the

trees and weighed. A sub-sample was then removed and placed in a plastic bag, sealed, labelled and stored in a cooler box. The height at which the first live branch occurred on the stem was recorded. All live branches were removed, weighed, labelled and stored as with the dead branches. The stem was also weighed with and without bark (Sale, 2001). A 5cm thick disc was removed from the stem at 40% of tree height. It was placed in a plastic bag, labelled, sealed and stored as with the other samples.

Stem profile measurements were made up the stem, both over-bark and under-bark. A tree stem is not a regular geometric shape (e.g. a cone or cylinder). Measurements therefore needed to be done in such a way as to take its irregular shape into account. Each tree was divided into segments, starting at the base. An initial mark was made at 1m from the ground (including stump height) and at two-metre intervals up the stem thereafter. Diameters were measured at each of these points both over and under bark, representing the central diameter of a two-metre cylinder. To calculate the volume of timber with top diameters equal to 0cm, 3cm, 5cm and 7cm respectively, the height to each of these top diameters as well as the under bark diameters at each of these points was measured. The distance between the 7cm top diameter and the end of the previous two-metre segment was also measured in field as a check.

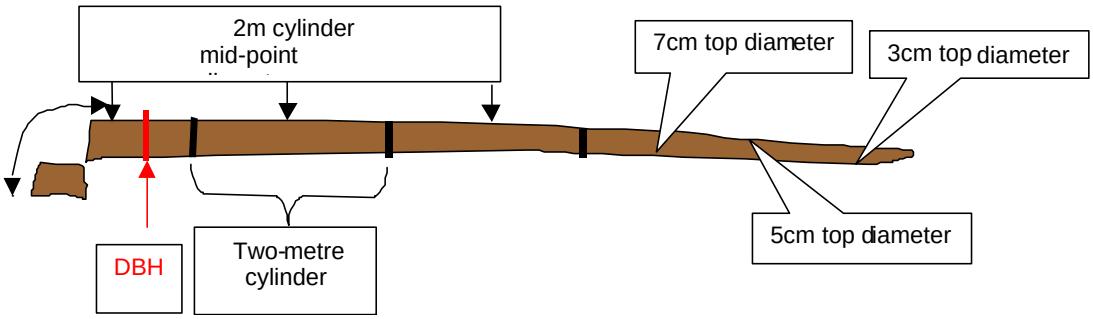


Figure 3: Diagram of measurement points along the stem.

Stem volume (over bark and under bark) to the various minimum top diameters, was then calculated using an appropriate series of cylinders.

3.2.2.2.2. Laboratory

Every evening after returning from the field, a sub-sample of thirty leaves was removed from the sample collected in field and weighed. These leaves were then glued to paper and photo copied (approximately 5 A4 pages per tree). The back of the paper was labelled. The remaining leaves and all the live-branches and dead branches were removed from their packets and the wet mass accurately recorded to one hundredth of a gram. These samples were then placed in brown paper bags, stapled closed and labelled (the mass of each brown paper bag was recorded beforehand). These brown paper bags were then placed in an oven at 70^{o}C until they reached a constant mass.

Once they had reached a constant mass at 70^{o}C, their dry masses were recorded.

The thickness of the disc at four points, perpendicular to each other, was recorded. The diameter of the disc was recorded with the bark on. The bark was then removed and the diameter of the disc without bark recorded. The wet mass of the disc and bark were recorded. The bark and the disc were placed into separate brown paper bags, stapled closed and placed in the oven to dry to a constant mass at 70^{o}C. The dry masses were then recorded.

3.2.2.3. Biomass fraction calculation

3.2.2.3.1. Leaves, stem, bark, live and dead branches

The dry mass of each fraction per tree could thus be calculated using the following equation:

$$\frac{SM_{Wet}}{SM_{Dry}} = \frac{TM_{Wet}}{TM_{Dry}} \therefore TM_{Dry} = \frac{SM_{Dry}}{SM_{Wet}} xTM_{Wet} \qquad \text{[Equation 8]}$$

where:

SM_{Wet} = Sample Mass Wet
SM_{Dry} = Sample Mass Dry
TM_{Wet} = Total Mass Wet (weighed in field)
TM_{Dry} = Total Mass Dry (what we are trying to calculate)

3.2.2.3.2. Leaf area

In order to calculate leaf area per tree the following equations were used:

$$\frac{SampLeafArea_{30}}{SM_{30dry}} = \frac{LeafAreaOfTree}{TM_{dry}} \therefore LeafAreaOfTree = \frac{SampLeafArea_{30}}{SM_{30dry}} xTM_{Dry}$$

[Equation 9]

where:

$SampLeafArea_{30}$ = Area of the 30 leaves.
SM_{30dry} = Dry mass of the 30 leaves (calculated using equation 10).
TM_{dry} = Total mass of dry leaves per tree (calculated using equation 8)
$LeafAreaOfTree$ = Total Leaf area of the tree.

With the 30 leaves having been glued to paper, it was not possible to directly measure their dry mass, which was therefore calculated using equation 10.

$$SM_{30Dry} = \frac{SM_{Dry}}{SM_{Wet}} xSM_{30Wet} \qquad \text{[Equation 10]}$$

where:

SM_{30dry} = Dry mass of the 30 leaves

SM_{30wet} = Wet mass of the 30 leaves
SM_{dry} = Dry mass of the main leaf sample
SM_{wet} = Wet mass of the main leaf sample

3.2.2.3.3. Wood Density

Was calculated as follows:

$$\frac{StemMass}{StemVolume} = WoodDensity(ton.m^{-3}) \quad \text{[Equation 11]}$$

or

$$\frac{DiscMass}{DiscVolume} = WoodDensity(ton.m^{-3}) \quad \text{[Equation 12]}$$

where:

StemMass = Mass of the stem (weighed in field)
StemVolume = Volume of stem calculated using stem profile measurements (as explained in (Sale, 2001)).
WoodDensity = Wood density
DiscMass = Mass of the disc measured in the laboratory (wet or dry)
DiscVolume = Volume of the disc calculated (using the average thickness from the four measurements and multiplying by the surface area (calculated from the diameter)). The immersion method of volume calculation would have been more accurate.

using:

Equation 11 to calculate the wet wood density in field

or

Equation 12 to calculate the dry or wet wood density using the disc (depending on whether the wet or dry mass is entered in the equation)

3.2.2.3.4. Bark Percentage

Was calculated as follows:

$$Bark\% = \frac{VolumeofBark}{VolumeofStemOverBark} x100 \quad \text{[Equation 13]}$$

where:

VolumeofBark = Volume of the Bark calculated from stem profile measurements (by subtracting volume under bark from volume over bark).
VolumeofStemOverBark = Volume of stem over-bark calculated from stem profile measurements.

3.2.2.3.5. Specific Leaf Area (SLA)

Can be calculated using:

$$SLA = \frac{SampLeafArea_{30}}{SM_{30dry}} \quad \text{[Equation 14]}$$

where:

SLA = Specific leaf Area
SampLeafArea$_{30}$ = Area of the 30 leaves.
SM$_{30dry}$ = Dry mass of the 30 leaves (calculated using equation 10).

3.2.2.3.6. Stem Volume

Stem volume was calculated by summing the volumes of each individual 2m cylinder for both under-bark and over-bark diameter (figure 3). The volume of the segment from the top of the last 2 m cylinder to the 7 cm over-bark, 5 cm over-bark and 3 cm over-bark top end diameters was then added to calculate the volume to the 7cm over-bark, 5cm over-bark, 3cm over-bark top end diameter, respectively. Full-tree volume was calculated by summing the volume of all the segments.

Measurement of replicate four and six was discontinued after they were destructively sampled at two and a half years and five and a half years respectively.

3.3. Mensurational Data Manipulation

3.3.1. Height:

The heights of those trees measured for DBH only, have been calculated using non-linear regression. The Gompertz growth function developed by Benjamin Gompertz in 1825 was deemed suitable, as it is an asymptotic function which means it does not allow the predicted height to decrease with an increase in DBH.

$$ht = b_0 + b_1 \times \exp(-\exp(-b_2(DBH - b_3))) \quad \text{[Equation 15]}$$

This function gave a better fit than the function conventionally used in South African forestry (Breedenkamp, 2000), namely:

$$\ln(ht) = b_0 + \frac{1}{DBH} \quad \text{[Equation 16]}$$

Separate sets of coefficients were generated for each treatment at each measurement age (Appendix 1). In the calculation of coefficients for the Gompertz function the constant (b_0) was omitted (origin made to pass through

zero). Goodness of fit was judged using the adjusted R^2 (indicates what percentage of the variance can be accounted for by the model) and the distribution of residuals across the size distribution of DBH. Equation 15 explained of 94.8 percent of the variance in height, whereas if the conventional function (Equation 16) was used, only 93.3 percent of the variance could be explained. Comparing the actual heights with the fitted heights calculated using the Gompertz function (Equation 15), and removing damaged trees (bent and broken tops) from the data set, gives an adjusted R^2 of 0.976 (see Figure 4). Due to both a higher adjusted R^2 and more even distribution of residuals across the DBH size range, the Gompertz function was chosen. The heights of all trees were then calculated using the Gompertz function, including trees that had actual height measurements. It was decided to replace measured values with calculated values in all later calculations involving height, to reduce the effect of error in the field measurement due to wind, bent trees, etc.

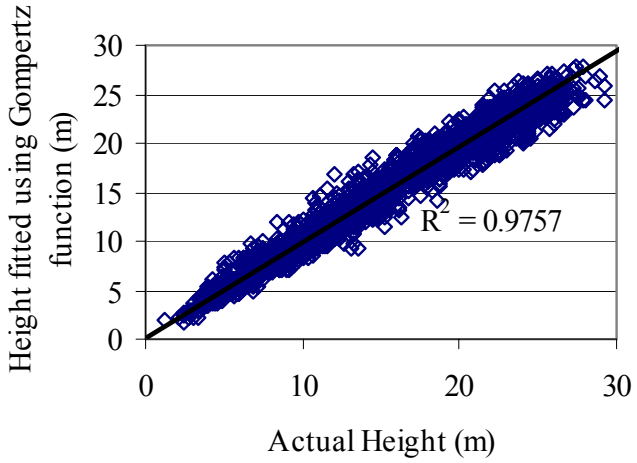


Figure 4: Relationship between actual height and predicted height for all measurement ages and treatments using the Gompertz function (damaged trees have been removed in this relationship).

3.3.2. Basal area:

Basal area is the cross-sectional surface area of the stem (including the bark) at 1.3m above the ground. It was calculated using:

$$\textit{Basal area} = \frac{\pi \times DBH^2}{4} \qquad \text{[Equation 17]}$$

The basal area of each measured tree was calculated. The individual basal area of each tree was summed per plot. This basal area per plot was then scaled up to basal area per hectare using:

$$\text{Basal area per hectare} = \frac{BasalAreaPerPlot}{PlotArea} \times 10000 \qquad \text{[Equation 18]}$$

3.3.3. Volume:

Direct measurement of volume can only be done destructively. Therefore numerous allometric equations have been developed using DBH alone or DBH and height as the independent variables. Volume data collected during the two destructive sampling events were used to generate coefficients for volume equations. Destructively sampled trees covered most of the size distribution encountered during the study period (the earliest measurements, therefore very small trees, were not covered). Both utilisable and full-tree stem volume are of interest in this dissertation, and therefore coefficients were generated for both. The standard volume equation form used in South African forestry is that developed by Schumacher and Hall.

$$\ln(Volume) = b_0 + b_1 \times \ln(DBH) + b_2 \times \ln(Height) \qquad \text{[Equation 19]}$$

where:

Volume = full-tree stem volume (m^3)

or

Volume = utilisable stem volume (m^3). Volume of stem up to an over-bark top diameter of 7cm.

The Shumacher and Hall equation was fitted using the coefficients derived by Coetzee (1992). Volume of individual trees was calculated using these coefficients and then compared to actual volumes calculated during destructive sampling. Ninety seven point three percent of the variation in actual volume was explained using the Coetzee (1992) coefficients for the Schumacher and Hall equation.

Coefficients for the Schumacher and Hall equation were then generated for both utilisable and full-tree stem volume, from the trees sampled during the two destructive sampling events. Only 89.1 percent and 96.4 percent of the variance could be accounted for when trying to calculate utilisable and full-tree stem volume respectively. Another volume equation was then tried, namely:

$$Volume = b_0 + b_1 \times DBH^2 \times Height \qquad \text{[Equation 20]}$$

Regression analysis showed that separate coefficients for the clone and the seedling did not increase the percentage of variance accounted for, and therefore only one set of coefficients was derived for volume calculation. When estimating the coefficients for utilisable stem volume, the origin was made to pass through zero as regression analysis showed that an estimated constant did not increase the precision of the model. The model for utilisable stem volume accounted for 98 percent of the variance. However when estimating the coefficients for full-tree stem volume, the constant did increase precision (97.9 percent of variance accounted for when constant was estimated, versus 97.7 percent of variance accounted for when origin was made to pass through zero). The estimated constant resulted in a positive y-intercept (this is however not possible, as a tree with no DBH or height will have no volume). When testing the results obtained using an estimated constant, it was found that the predicted volumes of very small trees (smaller

than those used to derive the coefficients) were severely inflated. It was therefore decided to have the origin pass through zero even though it reduced the precision of the model slightly. Due to the better fit obtained using equation 20, it was preferred to the Schumacher and Hall model. Equation 20 can now be expressed as:

$$VolumeFullTree = 0.000032228 \times DBH^2 \times Height \quad \text{[Equation 21]}$$

and

$$VolumeUtilisable = 0.000031068 \times DBH^2 \times Height \quad \text{[Equation 22]}$$

where:

VolumeFullTree = Full-tree stem volume (m^3)
VolumeUtilisable = Utilisable stem volume (m^3)

Stem volume (utilisable and full-tree) of each tree in the measured plot, at each measurement event, was then calculated using equation 21 and equation 22. These individual tree volumes were then summed on a per plot basis and scaled up to volume per hectare as follows:

$$VolHa = \frac{VolumePerPlot}{PlotArea} \times 10000 \quad \text{[Equation 23]}$$

where:

VolHa = Volume per hectare ($m^3.ha^{-1}$)

When calculating utilisable volume per hectare, trees with a DBH of less than 8 cm were excluded, as they do not produce at least one 2.4 m long log with a top end diameter over-bark of greater than 7 cm (which is the standard for minimum size on this plantation).

Chapter 4. Results

4.1. Stand growth characteristics

4.1.1. Height

4.1.1.1. Mean height ($\overline{ht}$) growth progression

The clonal treatments were significantly taller than the seedling treatments up to age 1 year. From age 1.9 years onward, the seedling treatments have been statistically significantly (p=0.05) taller than the clonal treatments (figure 5).

Table 1: Table of results from ANOVA's performed on $\overline{ht}$ over time

	F prob		
Age (yrs)	Initial Planting Density	Genotype	Genotype x Initial Planting Density
0.2	<0.001	0.367	0.128
0.4	<0.001	0.007	0.191
1	<0.001	<0.001	0.005
1.4	0.002	0.101	0.013
1.9	<0.001	<0.001	0.019
2.4	<0.001	<0.001	0.525
3.4	<0.001	<0.001	0.135
4.4	<0.001	<0.001	0.001
5	<0.001	<0.001	0.025
5.4	<0.001	<0.001	0.009

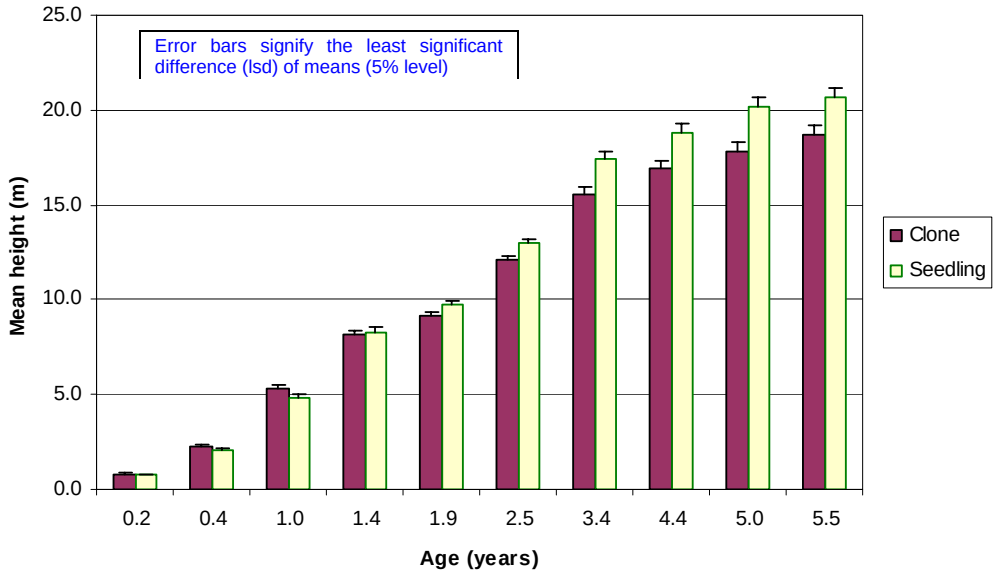


Figure 5: Mean height progression for each genotype over time

At an early age the highest planting densities had the largest mean height ($\overline{ht}$), with $\overline{ht}$ decreasing with decreasing planting densities. As time has progressed the rankings of $\overline{ht}$ have changed. The trend has been for rankings

to change in a regular pattern with the lower planting density treatments becoming progressively taller than the higher planting density treatments as time has progressed. Up to age 1 year the most densely spaced treatments were the tallest (figure 6). By age 5.5 years, the 1111 stems.ha^{-1}, 1587 stems.ha^{-1} and 2222 stems.ha^{-1} planting density treatments were the tallest, with no significant difference between them (p=0.05). The 6667 stems.ha^{-1} and 3333 stems.ha^{-1} treatments were the shortest and were statistically significantly different from one another (see figure 6).

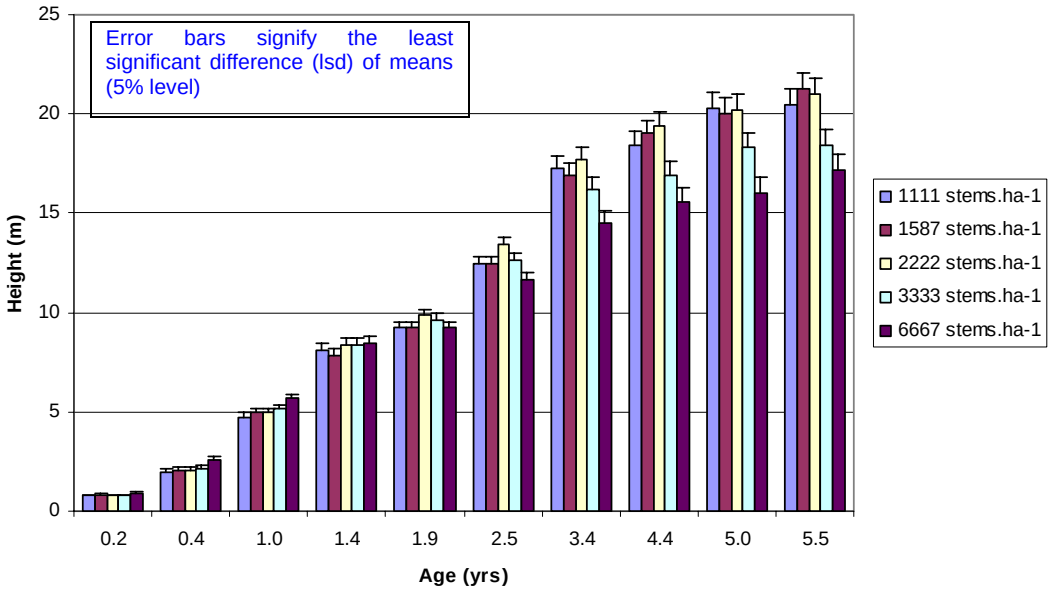


Figure 6: Mean height progression per planting density treatment over time

4.1.1.2. Variation in height over time

Variation within the population has been measured using the coefficient of variation (CV%). In both genotypes tested, there was initially a large degree of variation in height, followed by a sharp decrease in variation until reaching ages 1.4 years to 2.4 years. Thereafter there was a progressive increase in variation in all treatments (see figures 7 and 8). This is similar to the trend observed by Tomé *et al*. (1994), Bouvet (1997), Von Euler, Baradat and Lemoine (1992) and Little (1999).

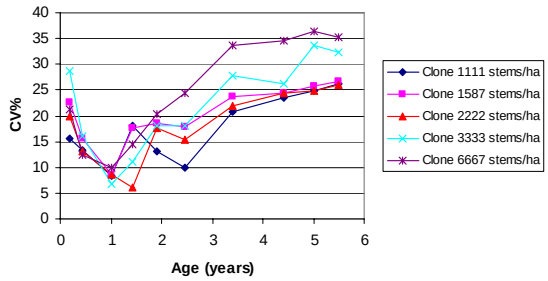


Figure 7: Change in coefficient of variation (CV%) over time for the clonal treatments

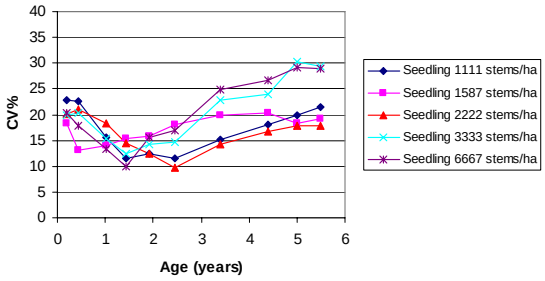


Figure 8: Change in coefficient of variation (CV%) over time for the seedling treatments

Table 2: Table of results from ANOVA's performed on CV% for height over time

	F prob		
Age (yrs)	Initial Planting Density	Genotype	Genotype x Initial Planting Density
0.2	0.204	0.335	.015
0.4	0.395	0.002	0.148
1	0.907	<0.001	0.726
1.4	0.174	0.654	0.072
1.9	0.211	0.028	0.866
2.4	<0.001	0.017	0.105
3.4	<0.001	<0.001	0.888
4.4	<0.001	<0.001	0.710
5	<0.001	<0.001	0.886
5.4	<0.001	<0.001	0.690

By age 5 years the variation in the higher planting density treatments, namely 6667 stems.ha^{-1} and 3333 stems.ha^{-1}, was statistically significantly greater (at the 5% level) than in the rest of the planting density treatments. There was no statistical difference in variation between the 2222 stems.ha^{-1}, 1587 stems.ha^{-1} and 1111 stems.ha^{-1} treatments (see figures 7 and 8). The clonal treatments (figure 7) displayed significantly greater variation than the seedling treatments (figure 8) from age 1.9 years.

4.1.1.3. Distribution of height within the population

Distribution of height within the population has been represented by means of skewness. A negative skewness is obtained when the mode is greater than the mean, and *visa versa*, a positive skewness is obtained when the mode is less than the mean.

Table 3: Table of results from ANOVA's performed on skewness for height over time

	F prob		
Age (yrs)	Initial Planting Density	Genotype	Genotype x Initial Planting Density
0.2	0.433	0.811	0.805
0.4	0.067	0.002	0.192
1	<0.001	0.335	0.338
1.4	0.018	0.414	0.001
1.9	<0.001	0.253	0.032
2.4	0.024	0.128	0.483
3.4	<0.001	0.355	0.128
4.4	<0.001	0.003	0.394
5	<0.001	<0.001	0.146
5.4	0.005	0.010	0.116

In figures 9 and 10 it can be seen that, similarly to CV%, the trend over time is for skewness to decrease sharply initially then increase. This is more pronounced in the clonal treatments than in the seedling treatments. From age 2.4 years the skewness in the seedling treatments (figure 10) remains virtually unchanged between -1.0 and -1.5, with the exception of the 6667 stems.ha^{-1} treatment, which increases from -1 to 0 by the age of 5.5 years. In the clonal treatments all planting densities tested display an increase in skewness over time from age 1.9 years, with the increase being most pronounced in the 6667 stems.ha^{-1} and 3333 stems.ha^{-1} treatments (figure 9).

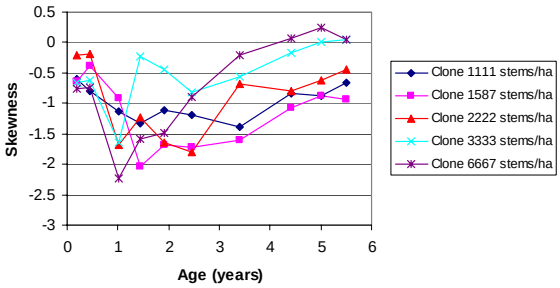


Figure 9: Change in population skewness for height over time for the clonal treatments

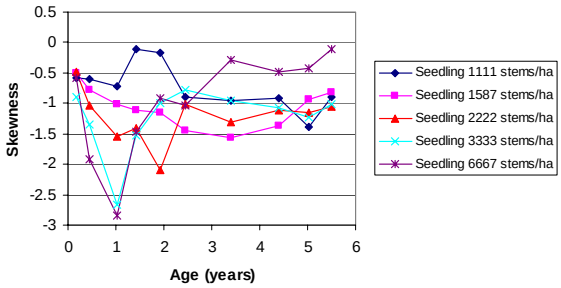


Figure 10: Change in population skewness for height over time for the seedling treatments

From age 4.4 years onward, the clonal treatments had a significantly (p=0.005) higher degree of skewness than the seedling treatments (see figures 9 and 10).

4.1.2. DBH

4.1.2.1. Mean DBH ($\overline{DBH}$) growth progression

Analysis of variance (ANOVA) results indicate that planting density is significant (at the 5% level) in explaining the variation in $\overline{DBH}$ from age 1 year (age of first $\overline{DBH}$ measurements), with an inverse relationship between $\overline{DBH}$ and planting density (see figures 11 and 12).

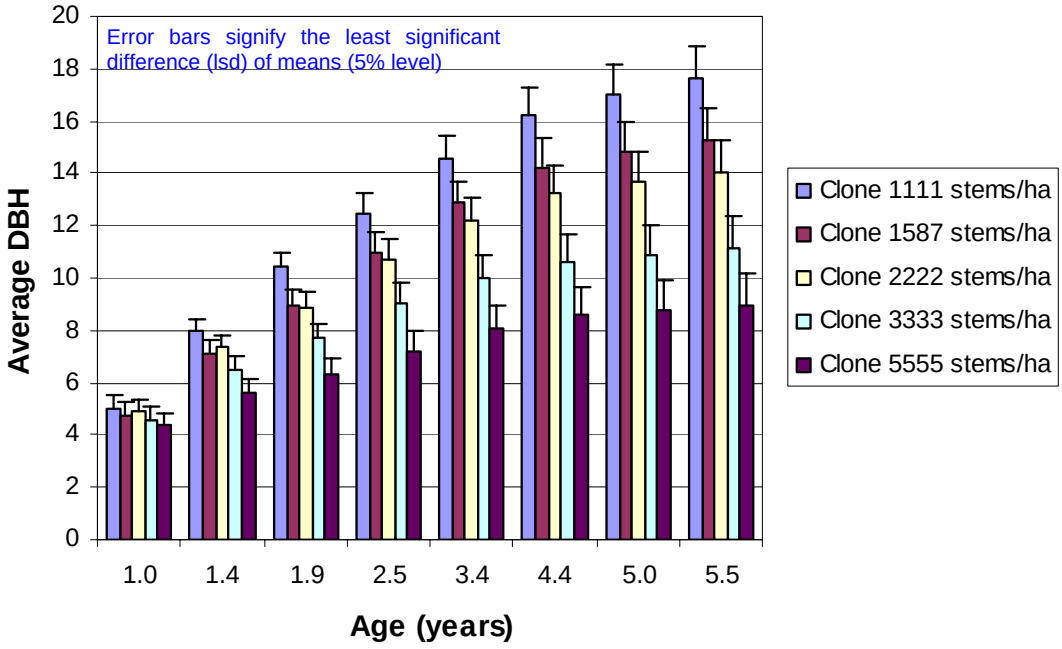


Figure 11: Progression of $\overline{DBH}$ over time for the clonal treatments

Genotype becomes significant in explaining the variation in $\overline{DBH}$ from age 3.4 years with the seedling producing significantly greater $\overline{DBH}$ than the clones.

Table 4: Table of results from ANOVA's performed on $\overline{DBH}$ over time

	F prob		
Age (yrs)	Initial Planting Density	Genotype	Genotype x Initial Planting Density
1	0.005	0.445	0.133
1.4	<0.001	0.262	0.216
1.9	<0.001	0.716	0.181
2.4	<0.001	0.097	0.926
3.4	<0.001	0.001	0.472
4.4	<0.001	<0.001	0.087
5	<0.001	<0.001	0.038
5.4	<0.001	<0.001	0.017

This is as a result of the $\overline{DBH}$ in the 6667 stems.ha^{-1} and the 3333 stems.ha^{-1} seedling treatments being significantly greater than those in the clonal treatments from age 3.4 years (see figures 11 and 12). From age 3.4 years there is an interaction between genotype and planting density. Even though this interaction is not significant at the 5% level (p = 0.087), the trend is for a larger range in $\overline{DBH}$ in the clonal treatments. The 1111 stems.ha^{-1} planting density clone treatments have a larger $\overline{DBH}$ than the seedling treatments of the same planting density and *visa versa* the seedlings have a significantly greater $\overline{DBH}$ in the 6667 stems.ha^{-1} and 3333 stems.ha^{-1} planting density treatments (see figures 11 and 12).

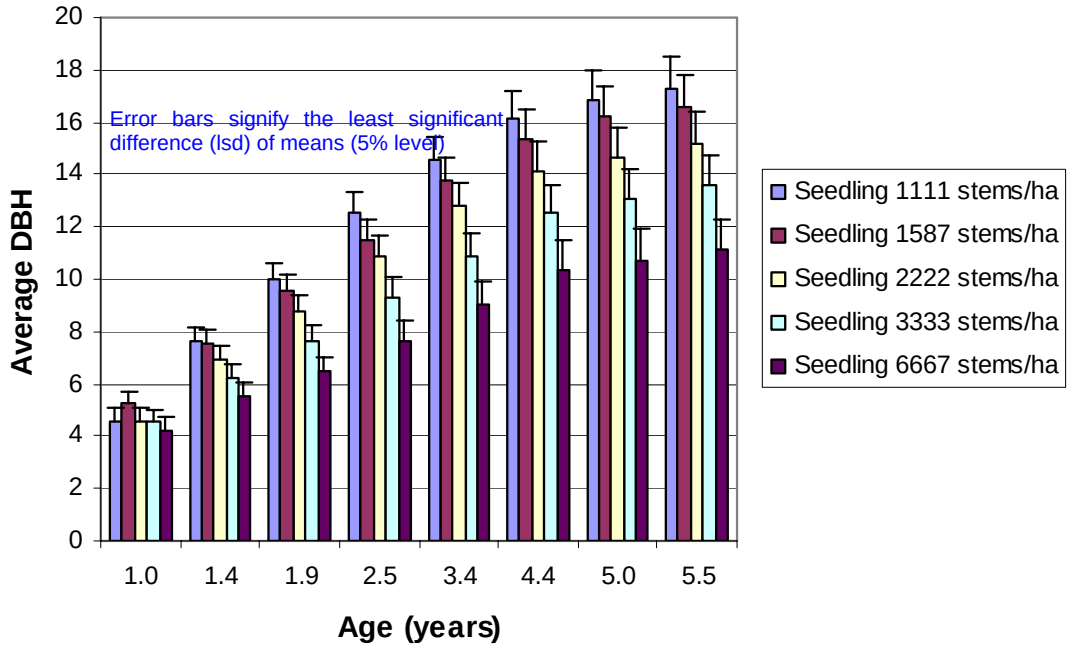


Figure 12: Progression of $\overline{DBH}$ over time for the seedling treatments

4.1.3. Basal area

4.1.3.1. Progression of mean basal area per tree ($\overline{BA}$)

As with $\overline{DBH}$, planting density is significant (5% level) in explaining the variation in $\overline{BA}$ from age 1 (see figures 13 and 14). Genotype became significant in explaining the variation in $\overline{BA}$ from age 3.4 years, with the seedling treatments having significantly greater $\overline{BA}$.

Table 5: Table of results from ANOVA's performed on $\overline{BA}$ over time

	F prob		
Age (yrs)	Initial Planting Density	Genotype	Genotype x Initial Planting Density
1	0.002	0.877	0.086
1.4	<0.001	0.189	0.172
1.9	<0.001	0.945	0.091
2.4	<0.001	0.176	0.857
3.4	<0.001	0.003	0.413
4.4	<0.001	<0.001	0.207
5	<0.001	<0.001	0.132
5.4	<0.001	<0.001	0.088

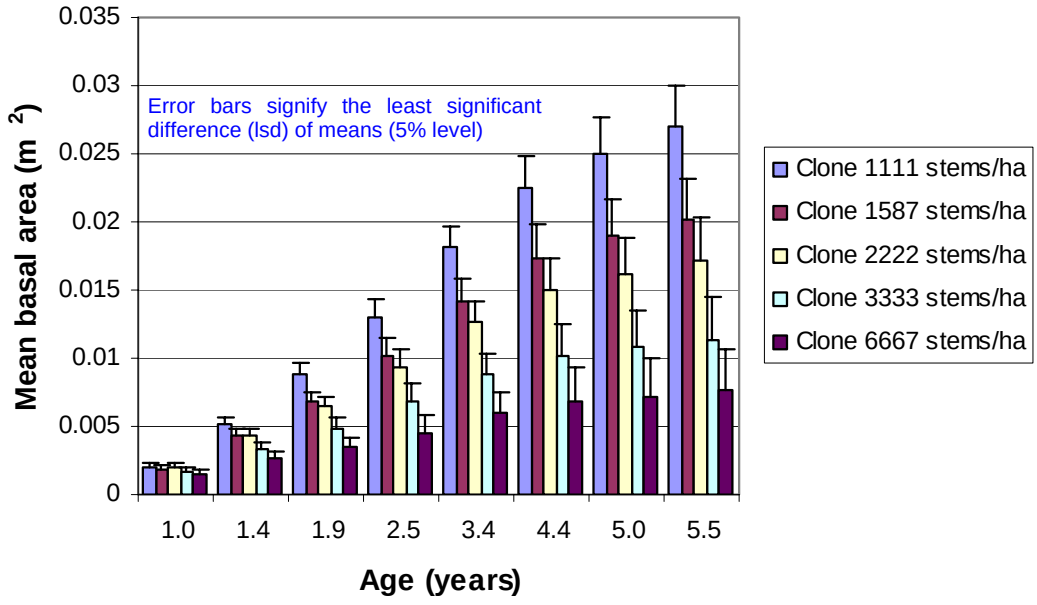


Figure 13: Progression of $\overline{BA}$ over time for the clonal treatments

The interaction between genotype and planting density only became apparent by age 5.5 years. Here the trend was a smaller range in $\overline{BA}$ within the seedling treatments, with the seedling treatments having significantly larger $\overline{BA}$ than the clones at higher initial planting densities (see figures 13 and 14).

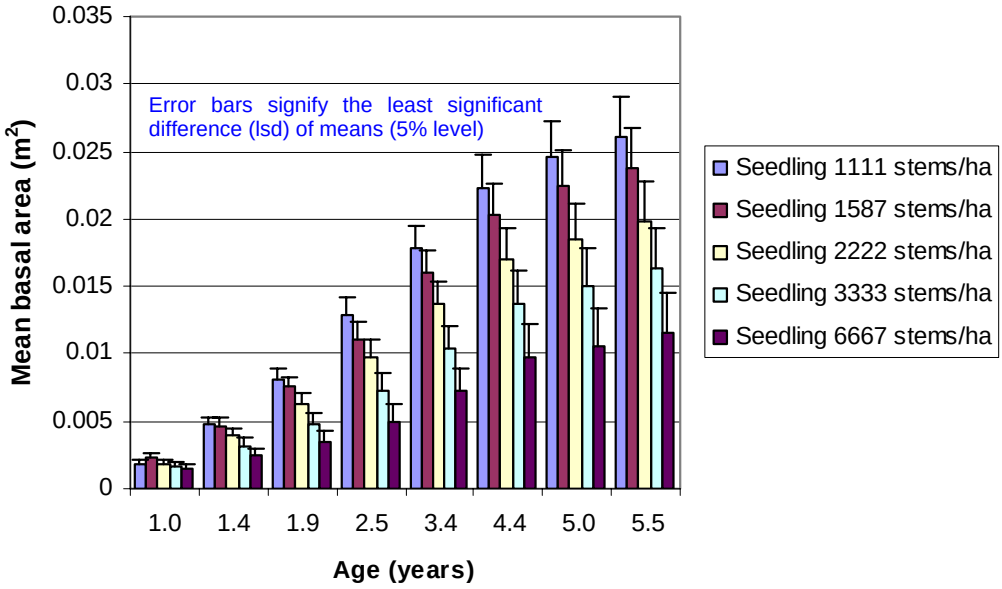


Figure 14: Progression of $\overline{BA}$ over time for the seedling treatments

4.1.3.2. Variation in basal area (BA) over time

Initially there was a low degree of between-tree variation. This variation was measured using the coefficient of variation (CV%). In the seedling treatments there was evidence of a decrease in the CV% from age 1 to 1.4 years, followed by an increase (see figure 16). This initial decrease was not evident in the clonal treatments (figure 15). As time has progressed, between-tree variation has increased. The rate of increase in between-tree variation has been determined mainly by planting density, with higher planting densities experiencing a more rapid increase in between-tree variation (figures 15 and 16). Initially the seedling treatments had more between-tree variation than the clonal treatments (significant at the 5% level at age 1 year). As time has progressed the clonal treatments have tended to have a greater amount of between- tree variation, with this difference being statistically significant by age 5.5 years.

Table 6: Table of results from ANOVA's performed on CV% for BA over time

	F prob		
Age (yrs)	Initial Planting Density	Genotype	Genotype x Initial Planting Density
1	0.422	<0.001	0.719
1.4	0.020	0.623	0.592
1.9	<0.001	0.559	0.359
2.4	<0.001	0.596	0.773
3.4	<0.001	0.341	0.798
4.4	<0.001	0.096	0.246
5	<0.001	0.054	0.227
5.4	<0.001	0.030	0.098

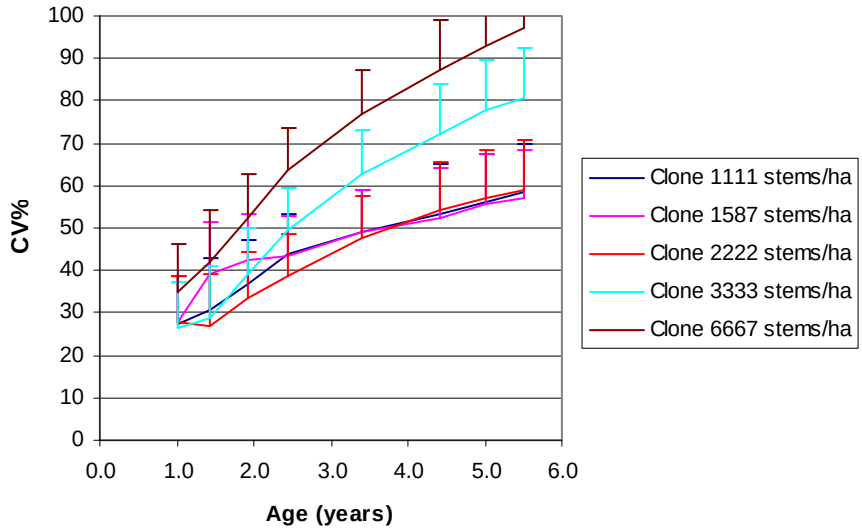


Figure 15: Progression of coefficient of variation for BA over time for the clonal treatments

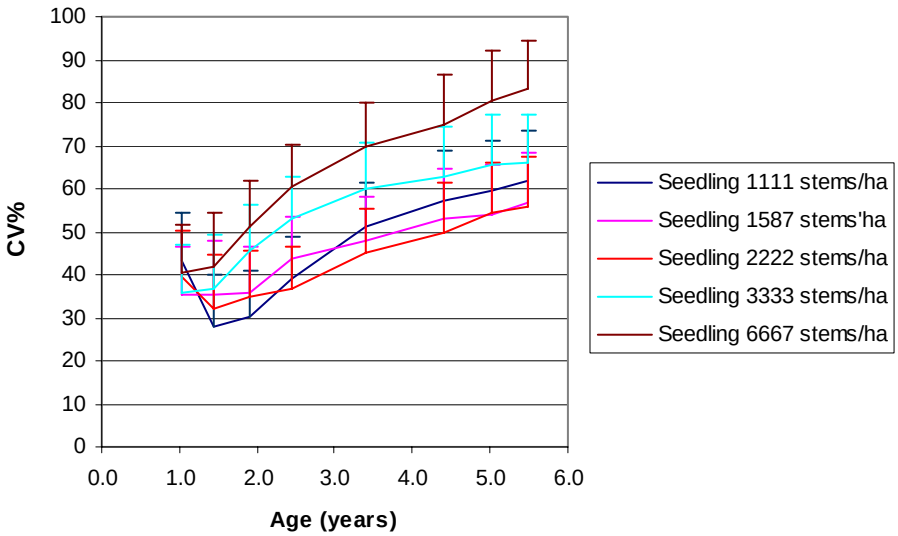


Figure 16: Progression of coefficient of variation for BA over time for the seedling treatments

Initially there was no obvious grouping of planting density treatments within genotypes. By age 3.4 years grouping of planting density treatments within genotypes had started to occur (three groups per genotype). In both the seedling and clonal treatments the 1111 stems.ha^{-1}, 1587 stems.ha^{-1} and 2222 stems.ha^{-1} treatments had grouped together (no significant difference between them at the 5% level), with the 3333 stems.ha^{-1} and 6667 stems.ha^{-1} treatments being statistically significantly different (5% level) from each other and all other treatments (see figures 15 and 16). In the clonal treatments these groupings remained until the last measurement at age 5.4 years (figure 15). In the seedling treatments the number of groups had been reduced to two by age 5, with the 3333 stems.ha^{-1} treatment no longer significantly different from the 1111 stems.ha^{-1}, 1587 stems.ha^{-1} and 2222 stems.ha^{-1} treatments (figure 16).

4.1.3.3. Distribution of BA within the population

The distribution of BA through the population has been examined using skewness. At ages 1.4 and 2.4 years the clone had a statistically significant more negative skewness than the seedling. At all other measurement events, there was no statistically significant difference between genotypes.

Table 7: Table of results from ANOVA's performed on skewness for BA over time

	F prob		
Age (yrs)	Initial Planting Density	Genotype	Genotype x Initial Planting Density
1	0.347	0.437	0.348
1.4	0.003	0.002	0.006
1.9	<0.001	0.136	0.377
2.4	<0.001	0.027	0.559
3.4	<0.001	0.118	0.117
4.4	<0.001	0.850	0.041
5	<0.001	0.828	0.036
5.4	<0.001	0.626	0.030

There was a trend of increasingly positive skewness with time and planting density, in both the seedling and the clone (figures 17 and 18). There was a larger range in skewness values observed between planting densities in the clone than in the seedling, at all measurement events except the first.

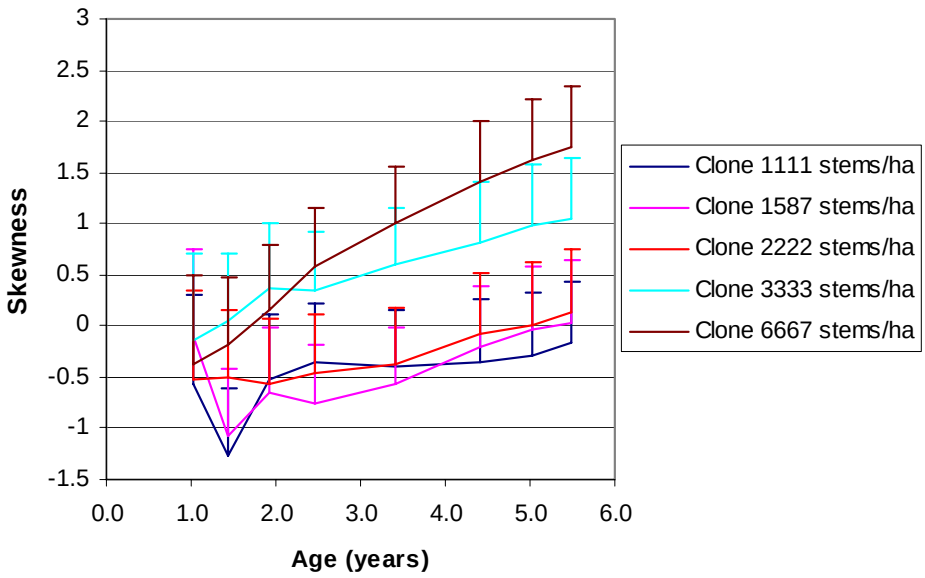


Figure 17: Progression of population skewness over time for the clonal treatments

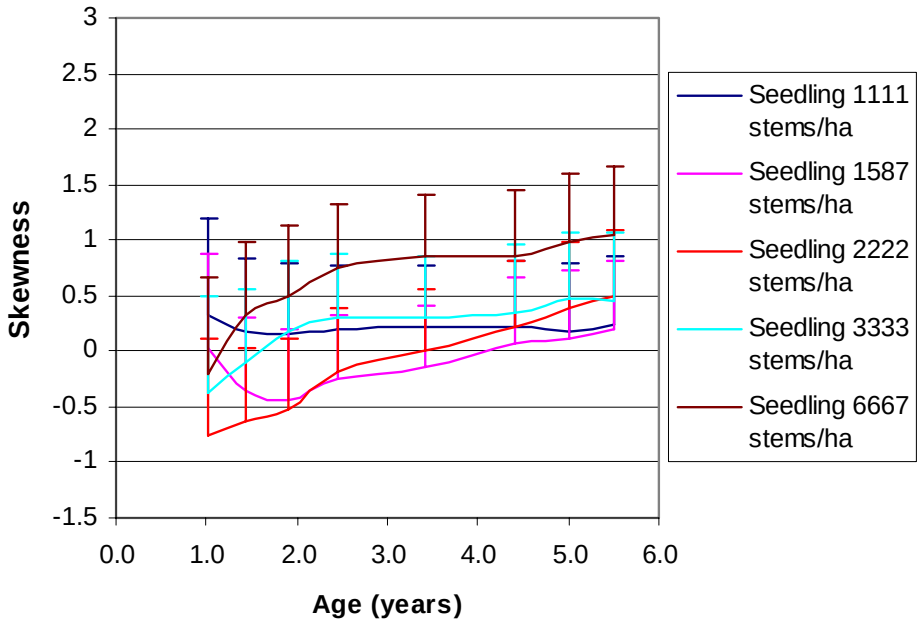


Figure 18: Progression of population skewness over time for the seedling treatments

From age 3.4 years onward there was a clear grouping of planting densities within genotypes. In the clonal treatments from age's 3.4 years to 4.4 years two groups had formed. By age 5 the clonal treatments had split in to 3 clear groups of planting densities, namely: i) 1111 stems.ha^{-1}, 1587 stems.ha^{-1} and 2222 stems.ha^{-1}, ii) 3333 stems.ha^{-1} and iii) 6667 stems.ha^{-1}. Each of these groups was statistically significantly different from the other (figure 17). In the seedling treatments, from age 3.4 years, two groups of planting densities had formed. This grouping remained the same until the last measurement event. The 1111 stems.ha^{-1}, 1587 stems.ha^{-1} and 2222 stems.ha^{-1} and 3333 stems.ha^{-1} treatments grouped together and were not significantly different from one another, with the 6667 stems.ha^{-1} treatment separating out and being significantly different from the rest (figure 18).

4.1.3.4. BA per hectare

From age 1 year the seedling treatments produced significantly greater BA per hectare than the clonal treatments (significant at the 5% level). Initial planting density was highly significant in explaining the variation in BA production per hectare from age 1 year. Higher initial planting densities have resulted in greater BA production per hectare at each age of measurement.

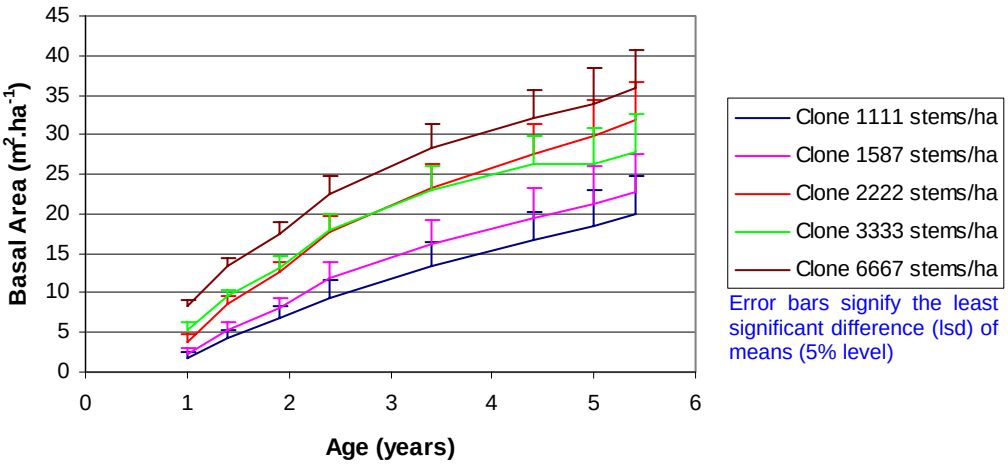


Figure 19: Progression of total BA per hectare over time for the clonal treatments

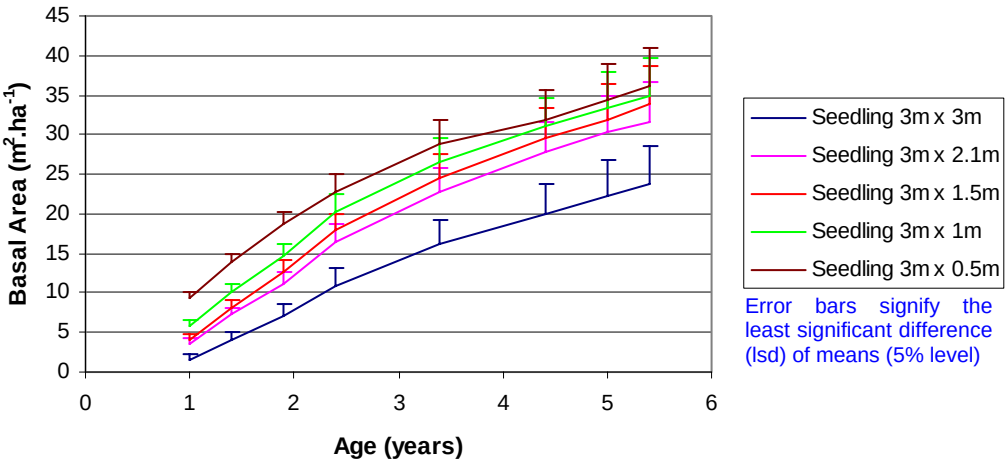


Figure 20: Progression of total BA per hectare over time for the seedling treatments

Table 8:Table of results from ANOVA's performed on BA.ha-1 over time

	F prob		
Age (yrs)	Initial Planting Density	Genotype	Genotype x Initial Planting Density
1	<0.001	0.006	0.075
1.4	<0.001	0.016	0.009
1.9	<0.001	<0.001	0.034
2.4	<0.001	<0.001	0.031
3.4	<0.001	<0.001	0.063
4.4	<0.001	<0.001	0.028
5	<0.001	<0.001	0.060
5.4	<0.001	<0.001	0.073

ANOVA's carried out for each measurement period show that there is an interaction between genotype and planting density on each occasion. This interaction is manifested through differential grouping of planting density treatments within each genotype. From age 1.4 years in the clonal treatments, three groupings of planting densities occur, namely: (i) 1111 stems.ha^{-1} with

1587 stems.ha^{-1}, (ii) 2222 stems.ha^{-1} with 3333 stems.ha^{-1} and (iii) 6667 stems.ha^{-1} (within these groupings there is no statistical difference between planting densities at the 5% level) (see figure 19). In the seedling treatments from age 2.4 in the seedling treatments, two groupings of planting densities start to manifest themselves, i.e. the 1111 stems.ha^{-1} treatment separates from the rest. From age 4.4 years there is no statistical difference (p=0.005) between planting density treatments within these groups (see figure 20).

4.1.4. Volume

4.1.4.1. Volume growth progression

From age 1.4 years onwards, full-tree volume production per hectare in the seedling treatments was statistically significantly (5% level) greater than in the clonal treatments. Planting density was highly significant (p<0.001) in explaining the variation in full-tree volume per hectare from age 1 year.

Table 9: Table of results from ANOVA's performed on full-tree volume.ha-1 over time

	F prob		
Age (yrs)	Initial Planting Density	Genotype	Genotype x Initial Planting Density
1	<0.001	0.111	0.053
1.4	<0.001	0.004	0.001
1.9	<0.001	<0.001	0.003
2.4	<0.001	<0.001	0.016
3.4	<0.001	<0.001	0.037
4.4	<0.001	<0.001	0.023
5	<0.001	<0.001	0.158
5.4	<0.001	<0.001	0.161

The clonal treatments exhibited a grouping of planting density treatments. However these groupings changed with time. Initially the two lowest planting density treatments, namely 1111 stems.ha^{-1} and 1587 stems.ha^{-1} grouped together and the 2222 stems.ha^{-1}, 3333 stems.ha^{-1} and 6667 stems.ha^{-1} treatments formed a second group. By age 4.4 these two groups had separated into four, with the 6667 stems.ha^{-1} and 2222 stems.ha^{-1} treatments forming one group and the other three planting density treatments forming individual groups. With the exception of the 3333 stems.ha^{-1} treatment, the higher the planting density the higher the full-tree volume production observed in the clone (figure 21).

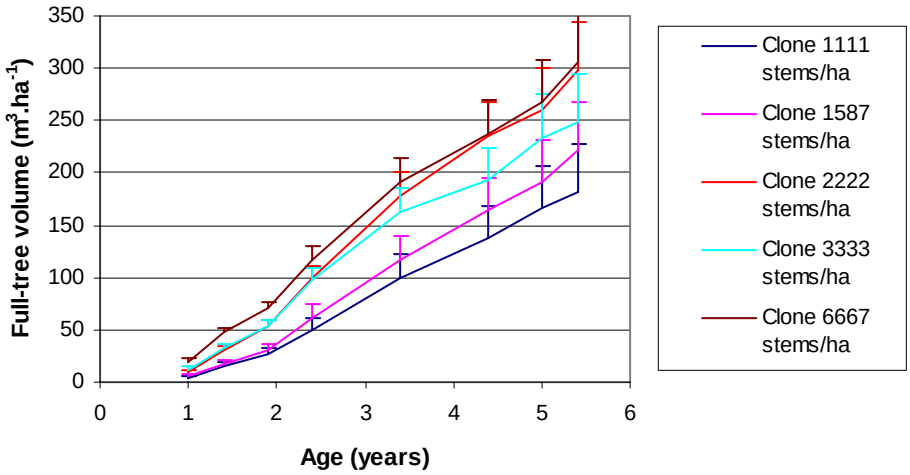


Figure 21: Progression of full-tree volume production per hectare over time for the clonal treatments

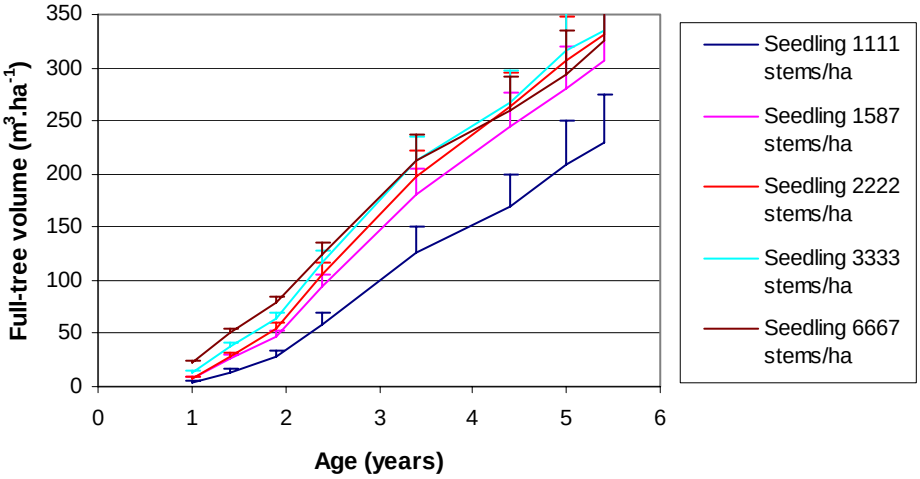


Figure 22: Progression of full-tree volume production per hectare over time for the seedling treatments

The seedling treatments exhibited a very distinct grouping of planting densities from age 2.4 years, with the 1587 stems.ha^{-1}, 2222 stems.ha^{-1}, 3333 stems.ha^{-1} and 6667 stems.ha^{-1} treatments grouping together. However, in contrast to the seedling treatments, these groupings did not change over time. By age 4.4 there was no statistically significant difference (5% level) between these treatments. The 1111 stems.ha^{-1} was always the lowest volume producing treatment (figure 22). It appears as though volume production is unaffected by planting density in the seedling treatments, unless some minimum planting density is not surpassed. Figure 22 suggests that this minimum planting density lies between 1111 stems.ha^{-1} and 1587 stems.ha^{-1} (3m x 3m and 3m x 2.1m respectively).

As with full-tree volume production, utilisable volume production in the clonal treatments appears to be more sensitive to planting density (larger spread of volumes resulting from a change in planting density) than the seedling treatments.

Table 10: Table of results from ANOVA's performed on full-tree volume.ha^{-1} over time

	F prob		
Age (yrs)	Initial Planting Density	Genotype	Genotype x Initial Planting Density
1.4	<0.001	0.305	0.014
1.9	<0.001	0.001	0.057
2.4	<0.001	<0.001	0.019
3.4	<0.001	<0.001	0.045
4.4	<0.001	<0.001	0.039
5	<0.001	<0.001	0.220
5.4	<0.001	<0.001	0.213

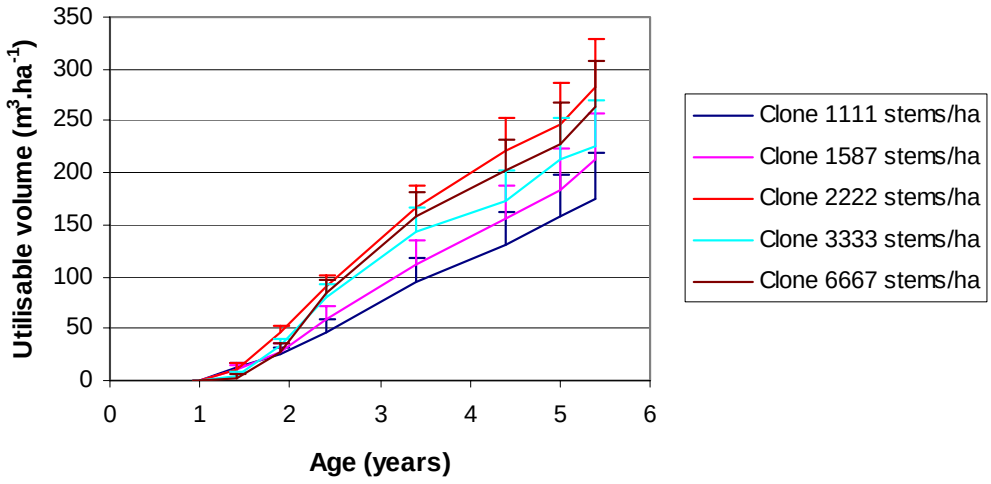


Figure 23: Progression of utilisable volume production per hectare over time for the clonal treatments

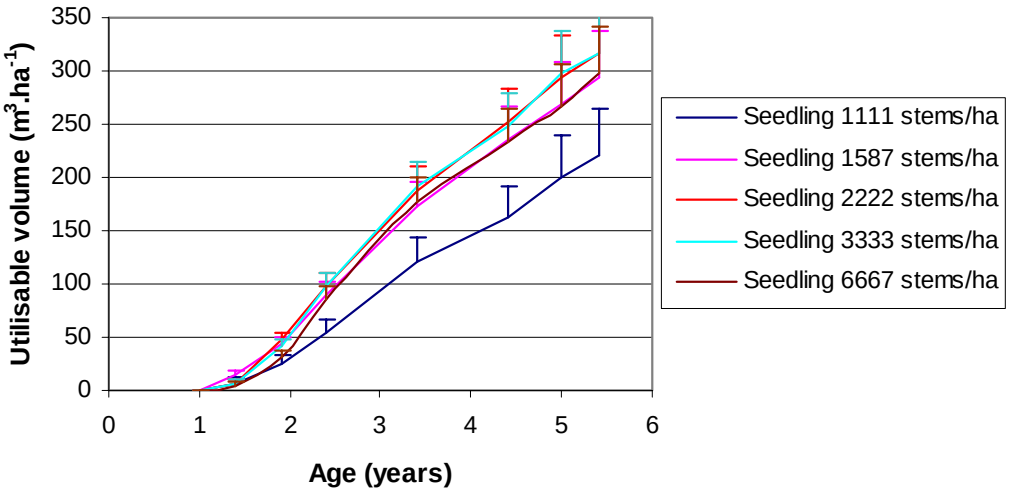


Figure 24: Progression of utilisable volume production per hectare over time for the seedling treatments

The seedling produces significantly more utilisable volume than does the clone from age 1.9 years onward. At the last measurement (age 5.4 years), the 2222 stems.ha^{-1} and the 1111 stems.ha^{-1} planting density treatments in both the seedling and the clone, were the most and the least productive respectively (figures 23 and 24).

4.1.4.2. Mean annual increment (MAI)

The MAI of full tree volume in the seedling treatments was statistically significantly (5% level) greater than in the clonal treatments from age 1.4 years onward. Planting density was highly significant ($p<0.001$ at the 5% level) in explaining the variation in full-tree MAI from age 1 year.

Table 11: Table of results from ANOVA's performed on full-tree volume MAI over time

	F prob		
Age (yrs)	Initial Planting Density	Genotype	Genotype x Initial Planting Density
1	<0.001	0.111	0.053
1.4	<0.001	0.004	0.001
1.9	<0.001	<0.001	0.003
2.4	<0.001	<0.001	0.016
3.4	<0.001	<0.001	0.037
4.4	<0.001	<0.001	0.023
5	<0.001	<0.001	0.158
5.4	<0.001	<0.001	0.161

The trend was for increased MAI as a result of increased planting density. There was a rapid increase in MAI up until age 3.4. Thereafter the MAI has remained stable or increased slightly. There was a slight dip in MAI in both genotypes tested at age 4.4 years. This resulted in a false peak in MAI at age 3.4 years. This dip was more apparent in the higher planting density treatments (figures 25 and 26) and is associated with the low rainfall received in the winter of 2001.

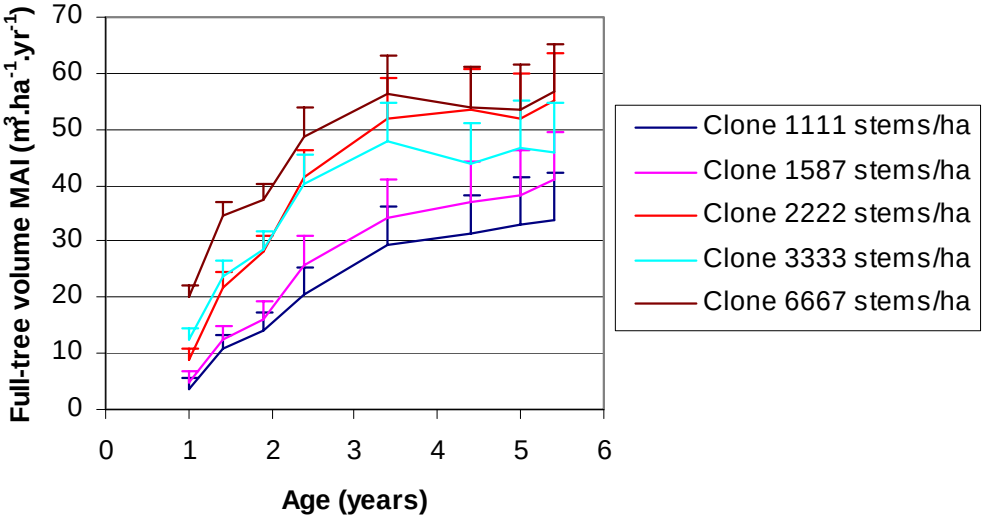


Figure 25: Progression of the mean annual increment of full-tree volume per hectare in the clonal treatments

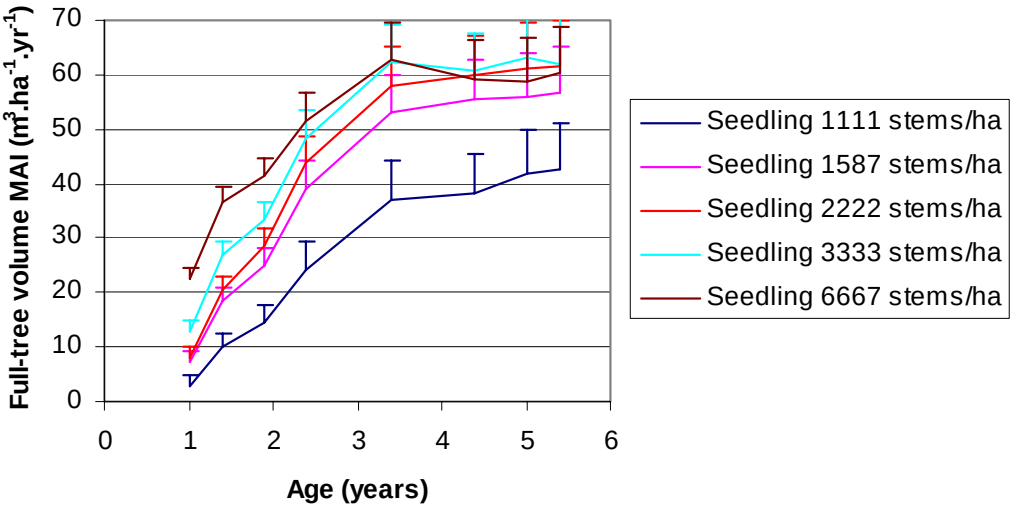


Figure 26: Progression of the mean annual increment of full-tree volume per hectare in the seedling treatments

As with full-tree volume there was a larger spread in MAI resulting from changes in planting density in the clonal treatments than in the seedling treatments. In the seedling treatments the four highest planting densities formed a very distinct group from age 2.4 onwards. There was no longer any statistical difference (5% level) between these treatments by age 4.4 years. There was however a highly significant ($p<0.001$ at the 5% level) MAI difference in the region of 15 to 20 $m^3.ha^{-1}.yr^{-1}$ between these four treatments and the 1111 stems.ha^{-1} planting density treatment.

When comparing the MAI of utilisable volume per hectare with the MAI of full-tree volume per hectare, two main differences are visible. There is less variation in utilisable MAI, as a result of different planting densities from age 1 year to age 2.4 years, than in full-tree MAI during the same period (see figures 25, 26, 27, 28).

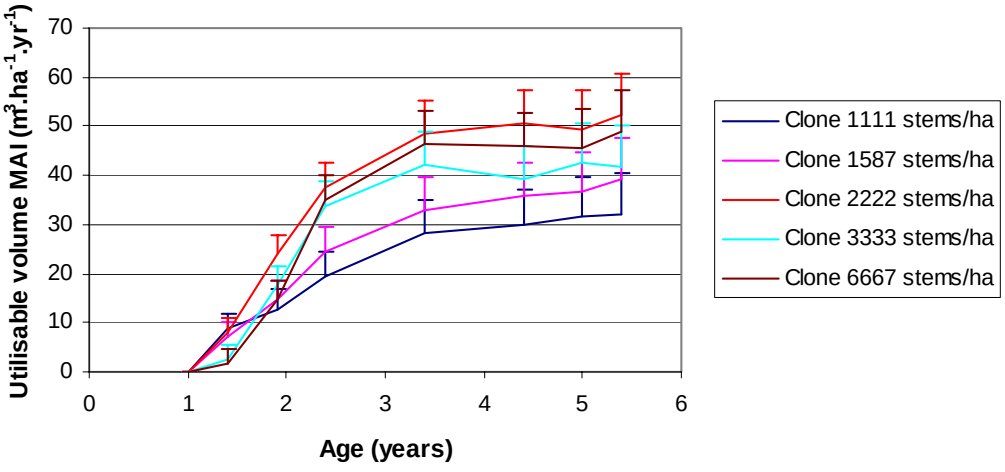


Figure 27: Progression of the mean annual increment of utilisable volume per hectare in the clonal treatments

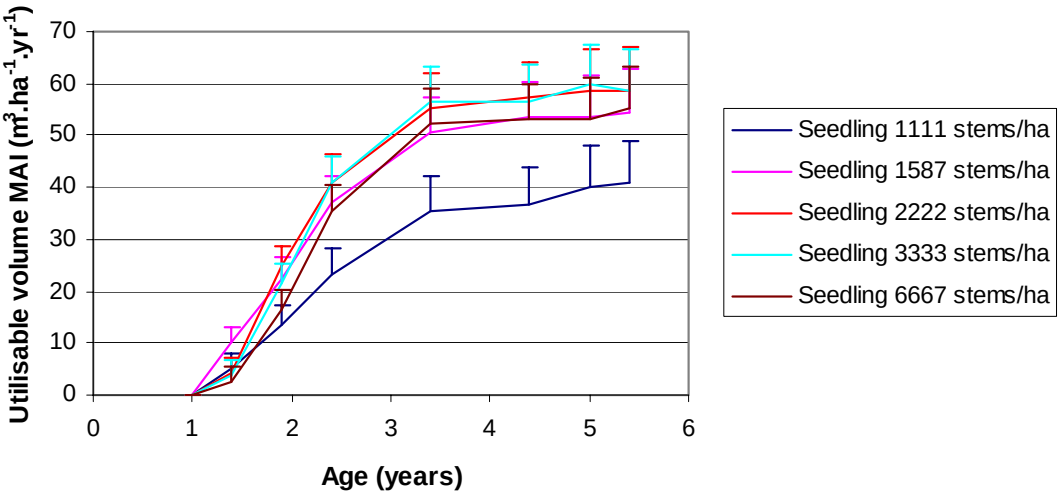


Figure 28: Progression of mean annual increment of utilisable volume per hectare in the seedling treatments

Table 12: Table of results from ANOVA's performed on utilisable volume MAI over time

	F prob		
Age (yrs)	Initial Planting Density	Genotype	Genotype x Initial Planting Density
1.4	<0.001	0.608	0.001
1.9	<0.001	0.001	0.057
2.4	<0.001	<0.001	0.019
3.4	<0.001	<0.001	0.045
4.4	<0.001	<0.001	0.039
5	<0.001	<0.001	0.220
5.4	<0.001	<0.001	0.213

The second difference is the less obvious dip in utilisable MAI at age 4.4 years, than in full-tree MAI. This difference is more pronounced in the seedling treatments where the dip is absent in utilisable MAI (see figures 26 and 28). The only possible explanation for this observed difference is a greatly reduced growth rate of small trees (< 8cm DBH) which are included in full-tree MAI but not in utilisable MAI.

4.1.4.3. Current annual increment (CAI)

From age 1.4 years to age 4.4 years the CAI of the seedling was statistically significantly greater than that of the clone, thereafter there was no significant difference between genotypes.

Table 13: Table of results from ANOVA's performed on full-tree volume CAI over time

	F prob		
Age (yrs)	Initial Planting Density	Genotype	Genotype x Initial Planting Density
1.4	<0.001	0.004	0.001
2.4	<0.001	<0.001	0.067
3.4	<0.001	<0.001	0.119
4.4	<0.001	<0.001	0.042
5.4	0.160	0.068	0.601

The full-tree volume CAI in both genotypes appeared to peak at age 3.4 years (figures 29 and 30). There was also a significant drop in CAI at age 4.4 years, which can be associated with drought conditions experienced in the winter of 2001. The amplitude of the peak experienced at age 3.4 years in the 6667 stems.ha^{-1}, 3333 stems.ha^{-1} and 2222 stems.ha^{-1} planting density treatments was significantly greater than that experienced by the two lower planting density treatments. The 6667 stems.ha^{-1} and 3333 stems.ha^{-1} experienced the greatest reduction in CAI with the onset of drought conditions experienced in 2001. By age 5.5 years the CAI of all treatments had increased from age 4.4 years, in response to improved rainfall. The increase in CAI from age 4.4 years to age 5.5 years was far greater in the 6667 stems.ha^{-1} and 3333 stems.ha^{-1} treatments than in the lower planting density treatments. Higher planting densities therefore appear to be the most sensitive to prevailing site conditions. The 1111 stems.ha^{-1} treatments had the lowest CAI throughout the life of the trial (figures 29 and 30).

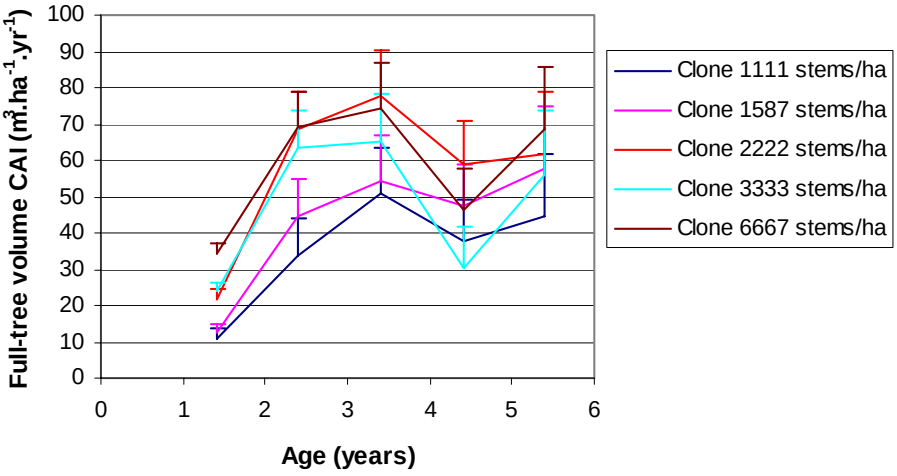


Figure 29: Progression of current annual increment for full-tree volume per hectare in the clonal treatments

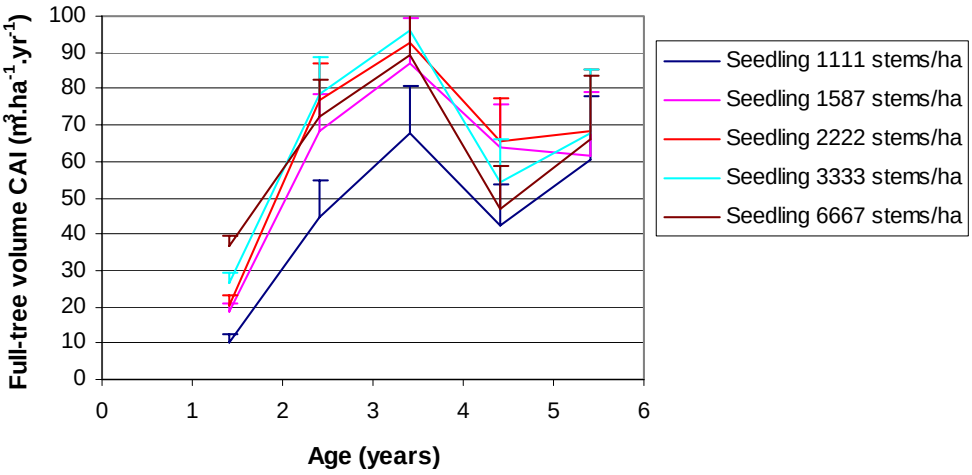


Figure 30: Progression of current annual increment for full-tree volume per hectare in the seedling treatments

From age 2.4 years to age 3.4 years two distinct groups of planting density treatments occur in both genotypes. In the case of the clonal treatments the three highest planting densities group together, and the two lowest planting densities group together (figure 29). In the seedling the four highest planting density treatments group together, and the 1111 stems.ha^{-1} treatment separates out on its own (figure 30). From age 4.4 years onward there is no distinctive grouping in either genotype. By age 5.5 years there is no statistically difference in CAI between any of the planting density treatments in the seedling (figure 30). By age 5.5 years in the clone only the 1111 stems.ha^{-1} planting density treatment has a statistically significant lower CAI, with the four highest planting density treatments grouping together (figure 29). In both genotypes, the 2222 stems.ha^{-1} treatments were able to both take advantage of better climatic conditions (part of the most productive group of treatments at age 3.4 years) and not experience the same decrease in CAI as the other treatments during drought conditions (figures 29 and 30).

When comparing the CAI of utilisable volume production with full-tree volume production, a number of differences become apparent. In the seedling treatments the large reduction in CAI in the 6667 stems.ha^{-1} and 3333 stems.ha^{-1} planting densities observed between ages 3.4 and 4.4 years, is less in the case of utilisable volume than full-tree volume (figures 30 and 32). CAI, especially in the higher planting densities, appears to peak earlier in the case of utilisable volume (age 2.4 years rather than age 3.4 years) (figures 31 and 32).

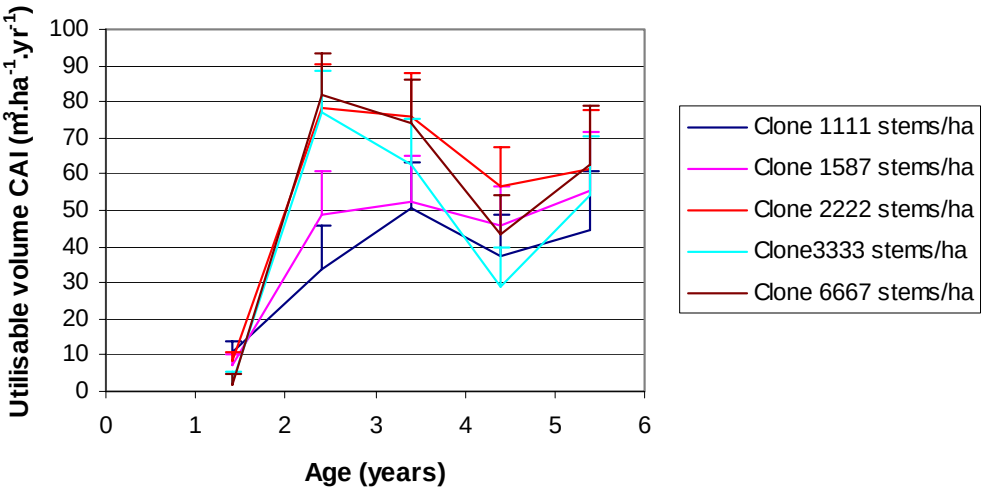


Figure 31: Progression of current annual increment for utilisable volume per hectare in the clonal treatments

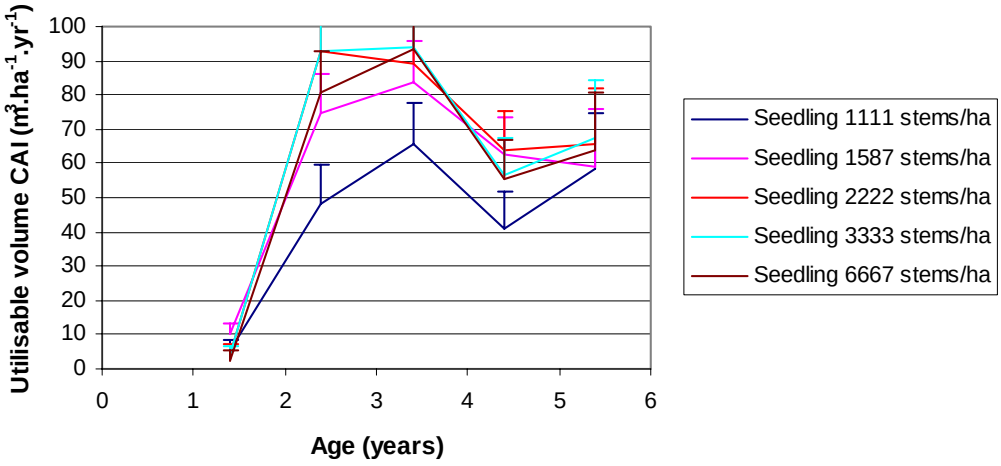


Figure 32: Progression of current annual increment for utilisable volume per hectare in the seedling treatments

In the seedling treatments the distinct grouping of planting densities observed up to age 3.4 years in the case of full-tree CAI, was maintained until age 4.4 years for utilisable volume CAI (figures 30 and 32).

Table 14: Table of results from ANOVA's performed on utilisable volume CAI over time

	F prob		
Age (yrs)	Initial Planting Density	Genotype	Genotype x Initial Planting Density
1.4	<0.001	0.608	0.001
2.4	<0.001	<0.001	0.079
3.4	<0.001	<0.001	0.142
4.4	<0.001	<0.001	0.041
5.4	0.147	0.036	0.635

4.1.5. Mortality/Survival

Survival percentages (survival %) were transformed for analysis purposes using the angular transformation (Gomez and Gomez 1984).

$$Transformation = \frac{180}{\pi} * \text{arc\_sine}\sqrt{\frac{\%}{100}} \qquad \text{[Equation 24]}$$

All analyses were based on transformed values, however for interpretation purposes, all graphs have been represented using untransformed values.

At age one, the survival in the seedling treatments was statistically (F pr<0.001) greater than that in the clonal treatments (figures 33 and 35). The average survival across all initial planting density treatments for the seedling was 94.9% (untransformed), whereas it was 83.7% (untransformed) in the clonal treatments. At age one year, neither initial planting density nor its interaction with genotype, could not explain a statistically significant portion of the variation in survival% (Table 15).

Table 15: Table of results from ANOVA's performed on transformed survival values from establishment based on transformed values

	F prob		
Age (yrs)	Initial Planting Density	Genotype	Genotype x Initial Planting Density
1	0.219	<0.001	0.212
1.4	0.004	<0.001	0.024
1.9	0.023	0.007	0.367
2.4	0.015	0.03	0.068
3.4	0.008	0.179	0.038
4.4	0.009	0.959	0.002
5	0.01	0.846	0.002
5.4	0.001	0.445	0.003

However, survival % is not the correct statistic to use when quantifying survival/mortality in spacing trials, as applying a percentage when the denominators are unequal (initial planting density), can confound the results.

When the absolute mortality was analysed (rather than a percentage), initial planting density and genotype, as well as their interaction were highly significant in explaining the variation at age one year (see table 16). The clonal 6667 stems.ha^{-1} initial planting density treatment suffered the greatest initial mortality of all treatments with 1432 trees.ha^{-1} dying in the first year. This number rose slowly to 2000 trees.ha^{-1} at age 4.4, and thereafter remained unchanged. For the rest of the clonal initial planting density treatments, there was a slight increase in mortality over time, from 271 trees.ha^{-1} to 481 trees.ha^{-1} between ages 1 and 5.5 years respectively. There was no statistically significant difference between these remaining treatments between ages 1 and 5.5 years.

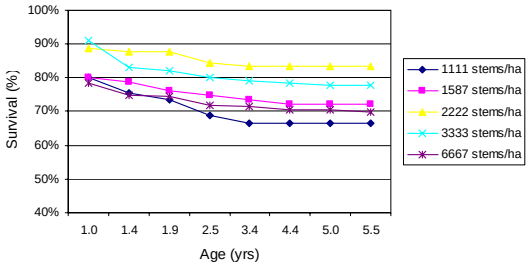


Figure 33: Survival % over time for the clonal treatments (untransformed)

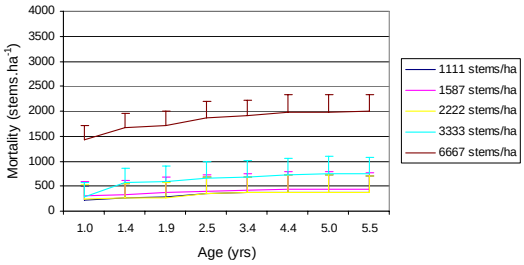


Figure 34: Progression of mortality over time from the date of establishment (clone)

The mortality experienced by the seedling 6667 stems.ha^{-1} initial planting density treatment by age 1 year was statistically greater than all the other seedling initial planting density treatments (494 trees.ha^{-1}). The mortality in this treatment continued to increase at a much higher rate than all the other treatments, and had reached 3506 trees.ha^{-1} by age 5.5 years. The mortality in all treatments increased over time. From age 1 year to age 2.5 years the 1111 stems.ha^{-1}, 1587 stems.ha^{-1}, 2222 stems.ha^{-1} and 3333 stems.ha^{-1} seedling initial planting density treatments did not differ from one another in a statistically significant manner. From age 3.4 onward, the mortality in the seedling 3333 stems.ha^{-1} initial planting density treatment increased to such

an extent that it became statistically greater than that in the 1111 stems.ha^{-1}, 1587 stems.ha^{-1} and 2222 stems.ha^{-1} treatments.

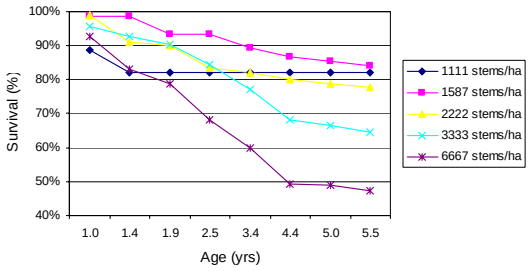


Figure 35: Survival % over time for the seedling treatments (untransformed)

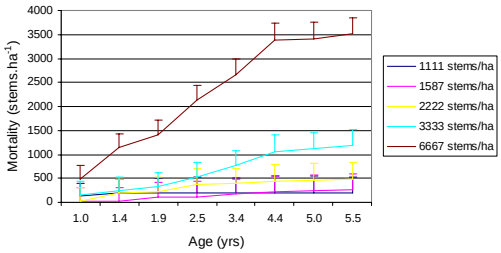


Figure 36: Progression of mortality over time from the date of establishment (seedling)

Table 16: Table of results from ANOVA's performed on mortality from establishment

	F prob		
Age (yrs)	Initial Planting Density	Genotype	Genotype x Initial Planting Density
1	<0.001	<0.001	<0.001
1.4	<0.001	0.001	0.233
1.9	<0.001	0.012	0.727
2.4	<0.001	0.447	0.318
3.4	<0.001	0.269	0.004
4.4	<0.001	<0.001	<0.001
5	<0.001	<0.001	<0.001
5.4	<0.001	<0.001	<0.001

The higher initial mortality in the clonal treatments can be attributed to the fact that at the time that this trial was planted there was very little knowledge or experience regarding planting techniques for clonal cuttings, especially in the Kwa-Zulu Natal Midlands.

If the effect of competition rather than establishment technique is the subject of this dissertation, then the effect of establishment mortality should be eliminated. To do this the mortality experienced after age one year was examined. This was done by quantifying the mortality experienced by age one and subtracting this from subsequent mortality figures.

When considering the mortality experienced after age one year, the difference between the seedling and clonal treatments become very clear. The overall trend is for mortality to increase over time in both genotypes. The clonal treatments experienced very little mortality from age one year onward. Between 123 and 568 trees.ha^{-1} had died by age 5.5 years. The 6667 stems.ha^{-1} and 3333 stems.ha^{-1} treatments had experienced more mortality than the other treatments. This difference has however not increased from age 2.5 years onward.

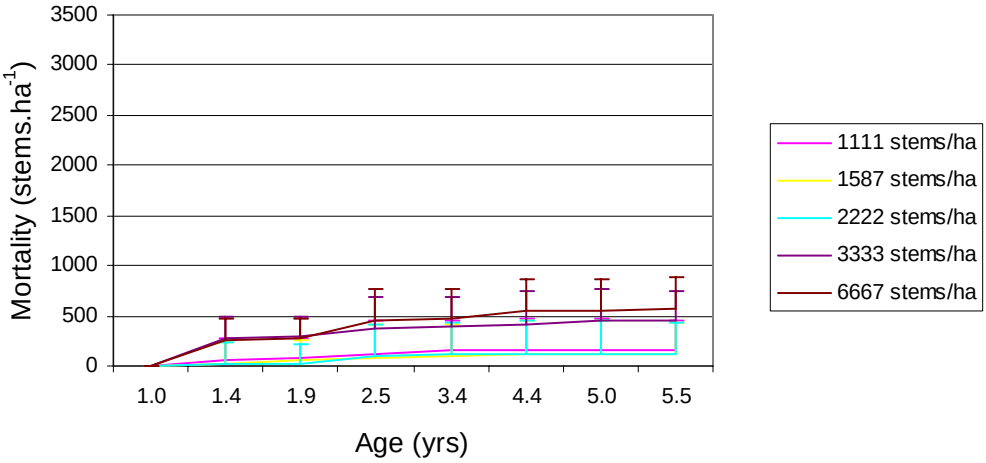


Figure 37: Number of trees to die after age 1 (clone)

In the seedling treatments the increase in mortality over time is greater than that in the clonal treatments. The trend is for mortality to be directly proportional to initial planting density. Within the seedling treatments, the differences in mortality between initial planting density treatments were marked. These differences became more significant as the trial aged.

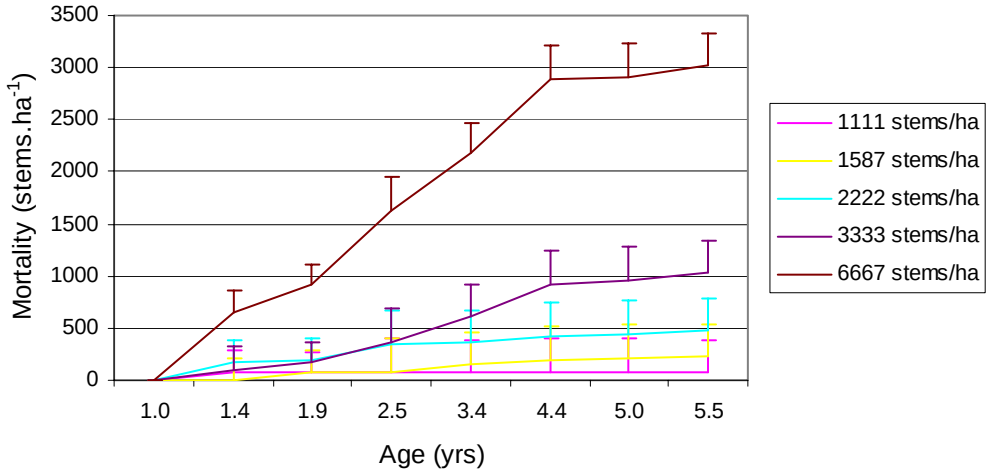


Figure 38: Number of trees to die after age 1 (seedling)

Table 17: Table of results from ANOVA's performed on mortality after age 1

	F prob		
Age (yrs)	Initial Planting Density	Genotype	Genotype x Initial Planting Density
1.4	<0.001	0.165	0.029
1.9	<0.001	0.010	<0.001
2.4	<0.001	<0.001	<0.001
3.4	<0.001	<0.001	<0.001
4.4	<0.001	<0.001	<0.001
5	<0.001	<0.001	<0.001
5.4	<0.001	<0.001	<0.001

4.1.5.1. Self-thinning

The self-thinning trend has been illustrated by graphically comparing individual tree size to survival. In figures 39 and 40 below, each line represents a plot, with the markers representing measurement events.

The relationship between survival and mean tree size is very different between the clonal and seedling treatments. In the seedling treatments, as time has progressed, an increase in mean tree size is associated with a decrease in survival (figure 39). It therefore appears that the growth of certain individuals is at the expense of the survival of others. The 1111 stems.ha^{-1} initial planting density treatment does not appear to be under the influence of intense competition, as individual tree size increase has not been at the expense of other trees.

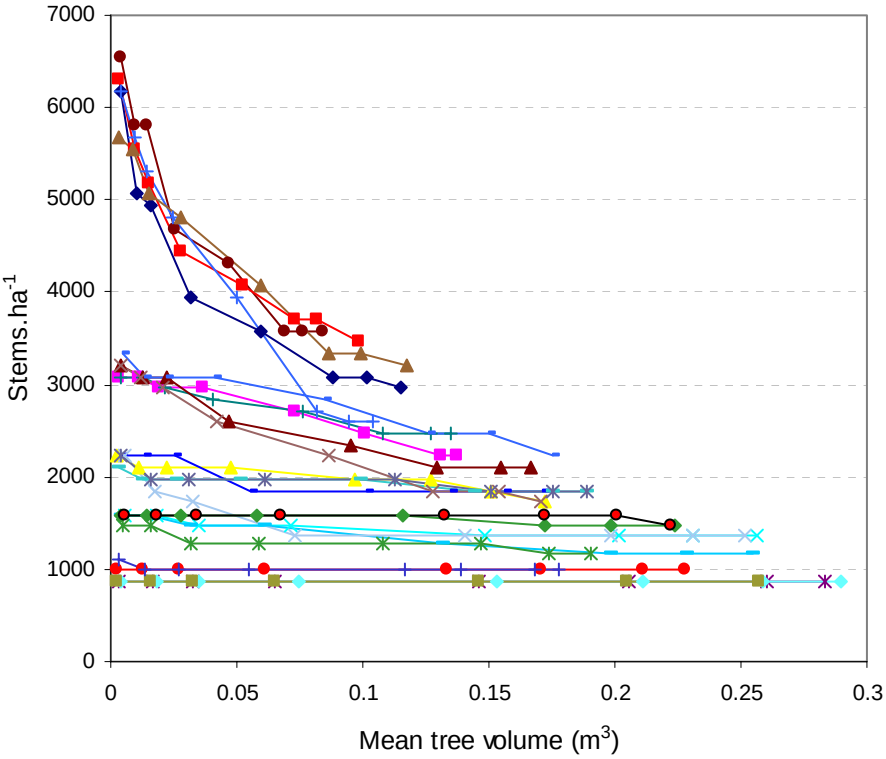


Figure 39: Relationship between mean tree volume and survival for all seedling plots

In the case of the clonal treatments, there has been little, if any, decrease in survival as individual tree size has increased. It therefore appears that as competition sets in for resources, the mean tree size increases only slightly, whereas survival does not decrease. It can therefore be stated that in the clonal treatments, survival occurs at the expense of individual tree growth.

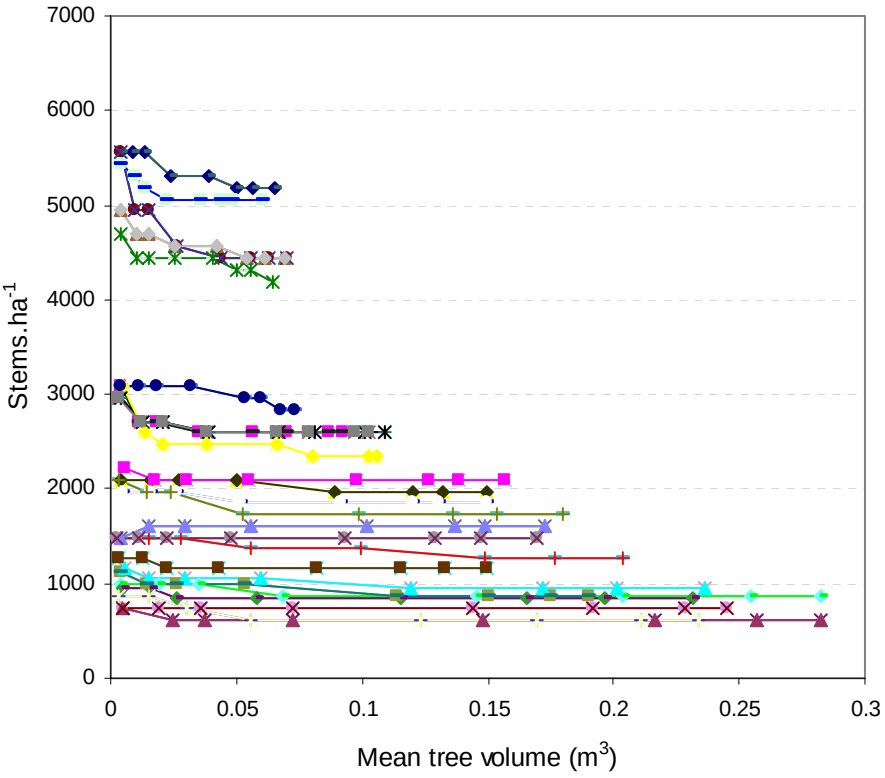


Figure 40: Relationship between mean tree volume and survival for all clonal plots

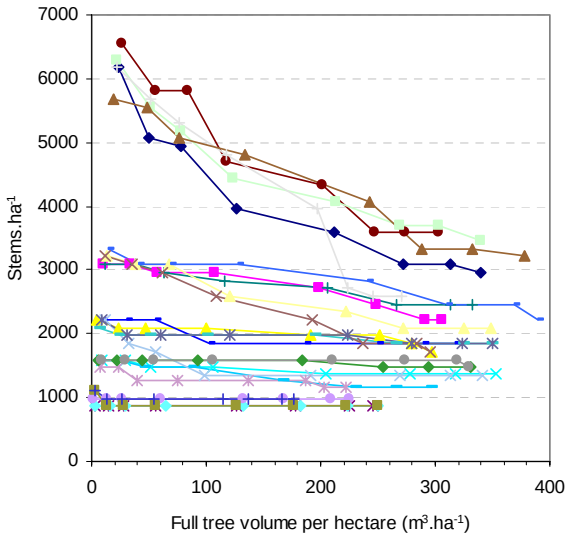


Figure 41: Relationship between full tree volume per hectare (plot level) and survival for all seedling plots

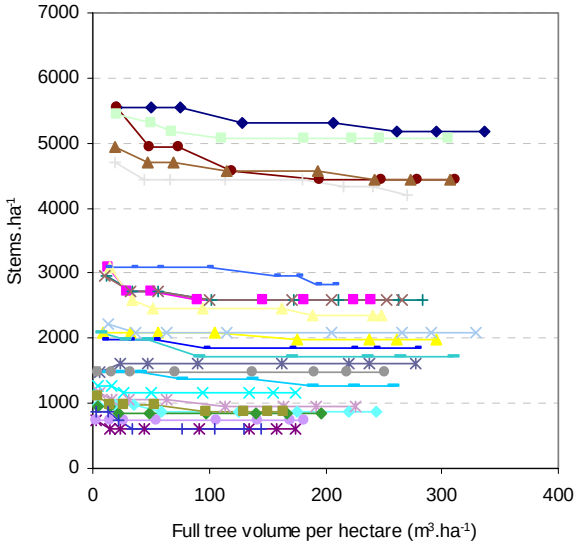


Figure 42: Relationship between full tree volume per hectare (plot level) and survival for all clonal plots

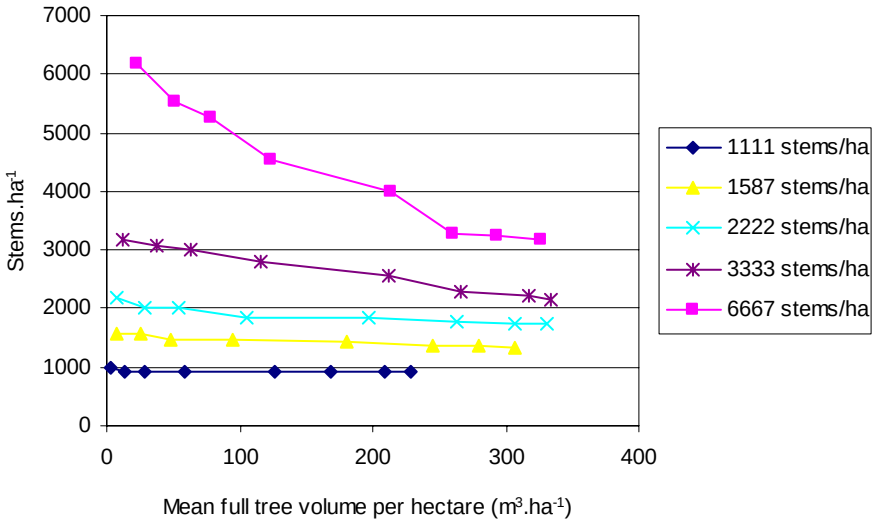


Figure 43: Relationship between mean full tree volume per hectare and survival for all seedling plots

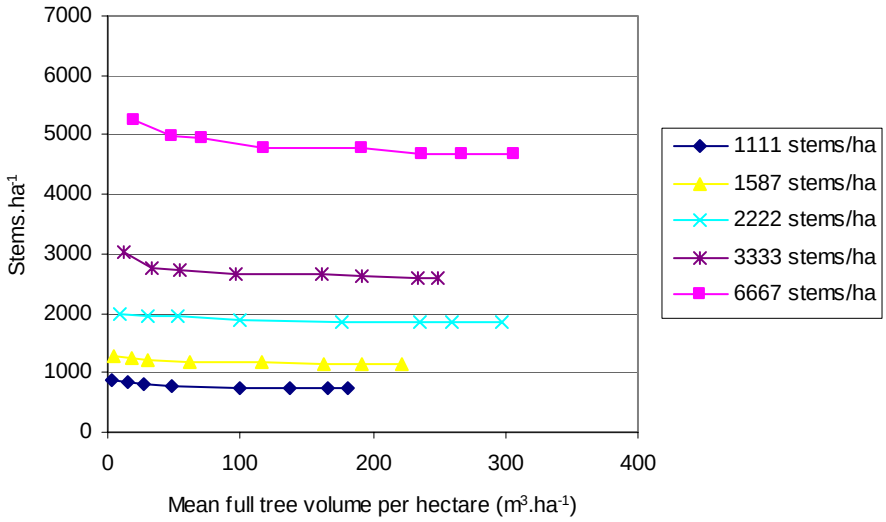


Figure 44: Relationship between mean full tree volume per hectare and survival for all clonal plots

4.2. Modelling of vigour

4.2.1. Choice of size variable (mass, volume, height, DBH or basal area) for modelling

Basal area was chosen as the size variable to be used, when modelling vigour for hypothesis testing.

Mass was not used as the size variable. It would have required destructive sampling at each measurement event. This destructive sampling would have destroyed too many replications within the trial and been prohibitively expensive and time consuming. Therefore mass was discarded as a variable to be used for modelling purposes.

Volume was also discarded as a potential size variable to be used for modelling purposes. Volume can be calculated using one of two methods; (i) direct measurement which is destructive, or (ii) through the use of DBH and height as inputs into an allometric equation for volume (see 3.3.3). Destructive measurement of volume was not considered for the same reason that direct mass measurement was not considered. Not all heights were measured (see 3.2.1), but modelled (see 3.3.1) using an allometric equation. There is a degree of error involved in estimating height from DBH. Furthermore there is a degree of error involved in estimating volume from DBH and height. This means that if modelling were to be done with volume, there would be three sources of error, namely: (i) estimation of height from DBH, (i) Estimation of volume from DBH and height (already has error) (iii) as well as the error involved in modelling volume. Therefore the use of volume as the size variable for hypothesis testing was discarded due the problem of mounting, and possibly compounding error.

DBH which has been measured directly for all the trees, could have been used, however it is a one dimensional variable. This means that it does not give a true reflection of stand occupancy. Therefore basal area was chosen as the size variable for modelling. The main reasons for this choice are summarised below:

a) Basal area is calculated directly from DBH. It is not modelled/estimated, and therefore there is no built in error to contend with while modelling.
b) Basal area is a two dimensional variable and therefore gives a good indication of stand occupancy, both at the individual tree and the compartment level.
c) Basal area was also the size variable, which behaved the most similarly to volume (which is the variable that industry is primarily interested in), when analysed in sections 4.1.3.4 and section 4.1.4.1.

4.2.2. Modelling methodology

The progression of DBH growth with time was modelled. Basal area was then calculated directly from DBH when necessary. The DBH growth of each measured tree was modelled through time by means of regression. The main growth function used was that developed by Benjamin Gompertz in 1825. This growth function was deemed suitable, as it is a sigmoidal asymptotic function, which means that it follows the growth pattern of all biological entities, and does not allow the predicted DBH to decrease with an increase in age. The coefficients for the equation were derived by means of non-linear regression analysis for each tree. The form of the equation is shown below:

$$DBH = A + C \times \exp(-\exp(-B(Age - M))) \qquad \text{[Equation 25]}$$

where:

A, *C*, *B* and *M* are coefficients generated per tree

and

A is a constant, which may or may not have been derived during the non-linear regression

For each individual tree the output from regression analysis was considered, firstly by looking at a graphical representation, to see if the line behaved in a logical way in relation to the points from which it was generated. Thereafter the goodness of fit statistics were analysed. Depending on the outcome from these two processes, it was decided whether to use the Gompertz function, with or without a constant, or some other function instead.

In order to derive the coefficients for the Gompertz function including a constant, at least 4 points are required. However 4 points will not allow for the goodness of fit statistics to be generated (too few degrees of freedom). Therefore ideally at least 5 points in time are required. If the Gompertz function is to be fitted without a constant, then at least 3 points are required. Again, using only three points does not allow for the generation of any goodness of fit statistics due to too few degrees of freedom. Therefore in this case ideally four points are required. The case of too few degrees of freedom was not considered to be a problem, as the growth of any individual tree will

never be modelled past the last point of measurement. Therefore these equations will never be used for extrapolation, but rather for modelling the growth trend between a finite set of points.

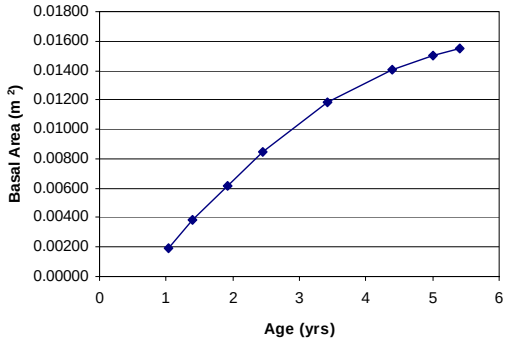


Figure 45: An example of the Gompertz function being fitted with a constant - tree number 7

Figure 46: An example of the Gompertz function being fitted without a constant - tree no 2

This function could however not be used in all cases. Some of the special cases have been detailed below:

a) When no DBH growth occurred from age 1 year onward, linear regression was used. A straight line with no gradient (b_1=0) and only a constant equal to the DBH at age 1 year was used (example figure 49).

b) In instances where the tree died after the first measurement, a linear model was used. Here only a constant was applied. And it was only relevant at age one year.

c) In instances where the tree died after the second measurement, the coefficients for a straight line (b_0 and b_1) between the two measurement events were derived.

d) In instances where the tree died after the third measurement and a straight line provided the best fit (rather than a Gompertz function without a constant), a straight line was used.

e) In some instances, a polynomial function provided the best fit. However visual inspection of the growth trajectory of the modelled line was inspected to ensure that the DBH never decreased with time within the study period for that tree (example figures 47 and 48).

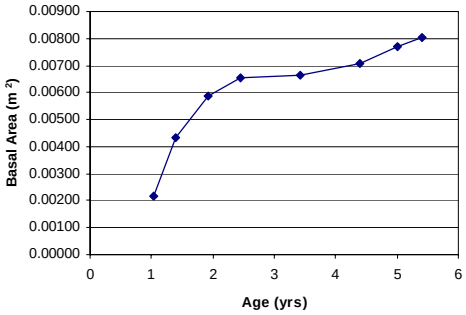


Figure 47: 4th order polynomial - tree 203

Figure 48: 3rd order polynomial - tree no 414

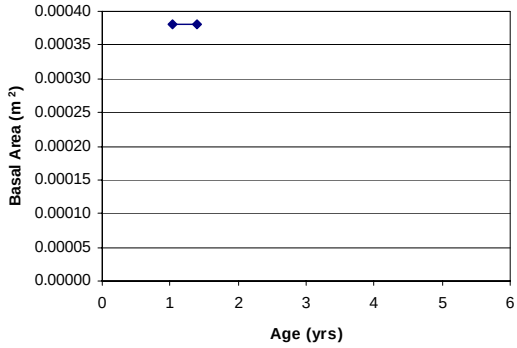


Figure 49: Straight line, no growth from age one, then dead by 2.5 - tree no 6

In some cases two regression models needed to be splined together, to best simulate the growth trend of the trees. Various combinations of growth functions/regression models were used. In some cases, the Gompertz function was splined with another Gompertz function, and in other cases the Gompertz function was splined with a straight line, or polynomial function. There were two main reasons for making use of more than one function for a specific tree:

a) Some trees would grow normally, with growth slowing and eventually stopping with time (this is what an asymptotic function simulates). Thereafter the growth rate would increase again (may be as a result of being released after the death of a neighbour dying). In these cases two growth functions were splined together. The age at which the changeover between growth functions occurs has been called a node. This node (age) was recorded where relevant, and used in the modelling process (example figures 50 and 51).

b) There were a few trees, which fell over early on in the life of the trial (most at age 1.4 years). These trees did not die. They sprouted epicormic shoots, of which a few later developed into trees. These “new” trees could not be ignored as they would use resources and compete with other trees, and therefore were relevant to the study. Therefore the growth of the tree was modelled before it fell over (usually a straight line as there were not enough points to fit the Gompertz function), and a separate regression

line used for after it re-sprouted (usually the Gompertz function) (example figures 52 and 53).

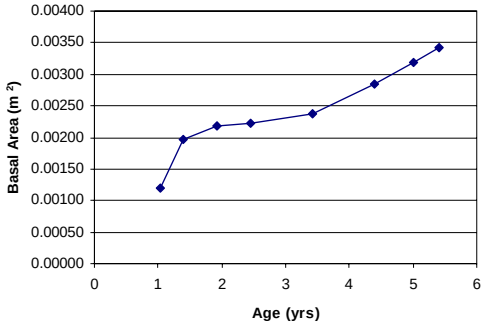


Figure 50: Two Gompertz functions splined at age 3.4 years - tree 361

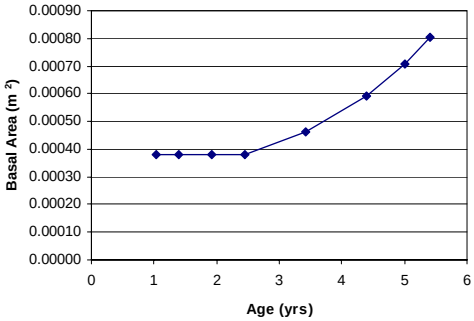


Figure 51: Straight line splined with Gompertz function at age 2.5 - tree 603

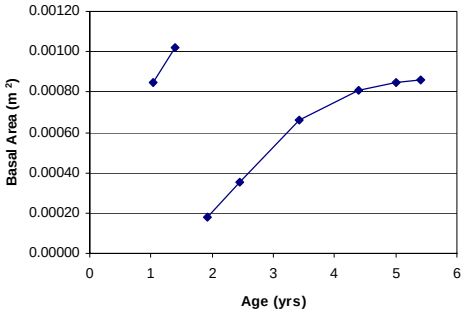


Figure 52: Tree grew to age 1.4, then fell over and re-grew (both straight line and gompertz functions used for one tree) - Tree 1111

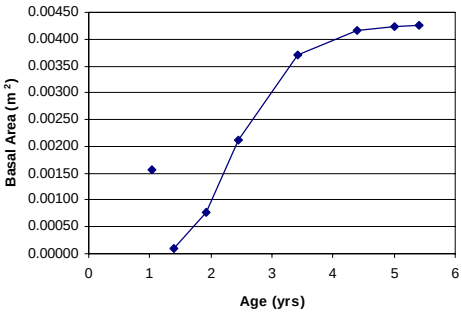


Figure 53: Tree fell over at age 1 then re-grew (point and Gompertz function combined for one tree) - tree no 209

If at any measurement event, it was discovered that a tree had died, this was recorded as the maximum age for modelling purposes. Therefore during modelling, no tree was allowed to grow past this maximum age.

4.2.2.1. Logic for individual tree growth

The results from the regression were stored in a Microsoft Access Database (see appendix 3). Modelling was done by means of a Microsoft Access query. Age was input via a specially designed form. The method and reasoning used in the query was as follows:

a) An age is entered as the independent variable

b) If this age is less that the maximum age for modelling then continue, otherwise there is no DBH (tree is dead)

c) Is the node age null?

d) If it is not null then is the input age less than or more than the node age?

e) If it is more than node age use the second set of coefficients, and *visa versa* if it is less than the node age use the first set of coefficients.

f) When using the first or second set of coefficients, is the constant for the Gompertz function null?

g) If not use the Gompertz function with a constant.

h) If it is null, but there are other Gompertz function coefficients present then use those.

i) If there are no Gompertz coefficients present then use the linear model coefficients in a linear model.

4.2.3. Modelling mean basal area growth

The average basal area of each plot was calculated at each measurement event. The Gompertz function was then used to model the progression of mean basal area, for each plot through time, using non-linear regression (see appendix 4 for table of coefficients). Ninety-nine point six and ninety nine point eight percent of the variance and sum of squares could be accounted for respectively.

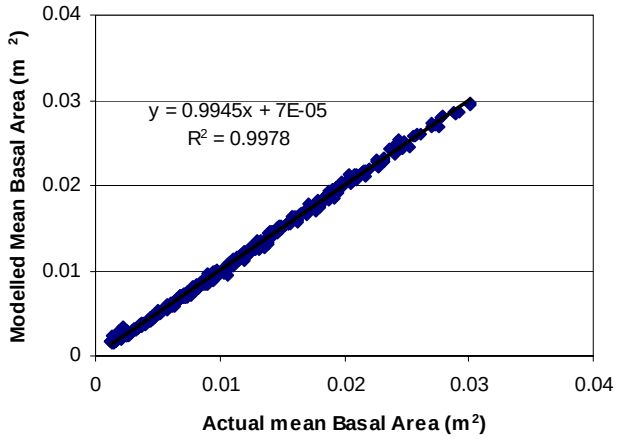


Figure 54: Modelled mean basal area vs. actual mean basal area

By making use of this equation it could be established at what age the mean basal area within a plot would have reached a certain size. This age could then be fed into the individual tree model for hypothesis testing.

4.2.4. Measures of vigour

Provision was made within the modelling framework to calculate near instantaneous growth rates. This was done by calculating the basal area of a tree at the model input age, as well as 0.1 years before, and 0.1 years after this model input age. By comparing the growth at the model input age with that 0.1 years before and after respectively, measures of vigour could be calculated as follows:

$$BAI_1 = \frac{BA_{(t)} - BA_{(t-0.1)}}{0.1}$$ [Equation 26]

$$BAI_2 = \frac{BA_{(t+0.1)} - BA_{(t)}}{0.1}$$ [Equation 27]

Relative Growth Rate (RGR) = $\frac{BAI_1}{BA_{(t-0.1)}}$ [Equation 28]

Relative production rate (RPR) = $\frac{\left(\frac{BAI_2 - BAI_1}{0.1 years}\right)}{BAI_1}$ [Equation 29]

where:

BAI = Mean Basal Area Increment
BA(t) = Basal Area at model input age
$BA_{(t-0.1)}$ = Basal area at model input age minus 0.1 years
$BA_{(t+0.1)}$ = Basal area at model input age plus 0.1 years

4.2.5. Hypothesis testing

4.2.5.1. Hypothesis 1

The variation in vigour between planting densities, genotypes and their interaction was analysed. The analysis was performed at three equal mean tree sizes (basal area), namely; (i) 0.007 m^2, (ii) 0.009 m^2 and (iii) 0.015 m^2. Using the model developed for mean basal area (section 4.2.3), the ages at which each plots mean basal area equalled 0.007 m^2, 0.009 m^2 and 0.015 m^2 was calculated. These ages were then inserted into the individual tree models (section 4.2.2). The individual tree models were then used to calculate various measures of vigour, namely: relative growth rate (RGR) and relative production rate (RPR). These measures of vigour were calculated for each tree. The results for each tree were summarised per plot and these values compared using analysis of variance. At a mean tree basal area of 0.007 m^2 all planting density treatments could be compared. At 0.009 m^2 the 6667 stems.ha^{-1} treatments had to be excluded from the analysis, as the 6667 stems.ha^{-1} clonal plots do not reach this mean basal area within the study period (figure 13). Whilst analysing vigour at 0.015 m^2 mean basal area both the 6667 stems.ha^{-1} and the 3333 stems.ha^{-1} treatments had to be excluded, because the clonal 6667 stems.ha^{-1} and the 3333 stems.ha^{-1} treatments did not reach this size within the study period (figure 13).

Table 18: Results from ANOVA for various measures of vigour, at various mean basal areas.

		F pr.		
Measure of Vigour	Mean Basal Area	Planting Density	Genotype	Planting Density x Genotype
RGR	0.007 m^2	<0.001	0.478	0.306
	0.009 m^2	<0.001	0.313	0.411
	0.015 m^2	<0.001	0.843	0.154
RPR	0.007 m^2	<0.001	0.801	0.872
	0.009 m^2	<0.001	0.486	0.926
	0.015 m^2	0.528	0.916	0.988

In all instances, with the exception of RPR at 0.015 m^2 mean basal area, initial planting density was highly significant (F pr. <=0.001) in explaining the variation in vigour (table 18). Neither genotype nor its interaction with initial planting density could explain a statistically significant portion of the variation in vigour. There was a clear inverse relationship between initial planting density and vigour (figures 55 and 56). The mean relative production rates in plots with an initial planting density of 1111 stems.ha^{-1} or 1587 stems.ha^{-1} are statistically significantly greater than that in plots with initial planting densities of 6667 stems.ha^{-1} or 3333 stems.ha^{-1} (figure 55) at a mean basal area of 0.007m^2.

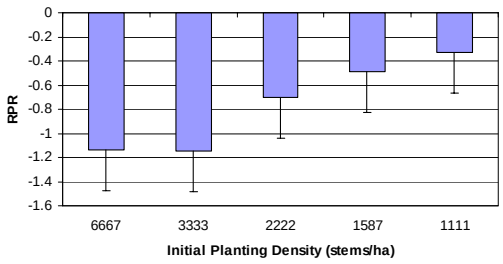


Figure 55: Mean RPR for plots at mean basal area of 0.007 m^2

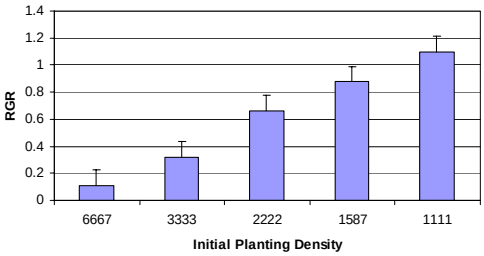


Figure 56: Mean RGR for plots at mean basal area of 0.007 m^2

At 0.009 m^2 mean basal area the mean RPR and mean RGR of the 1111 stems.ha^{-1} and 3333 stems.ha^{-1} treatments are statistically significantly different from one another (figures 57 and 58).

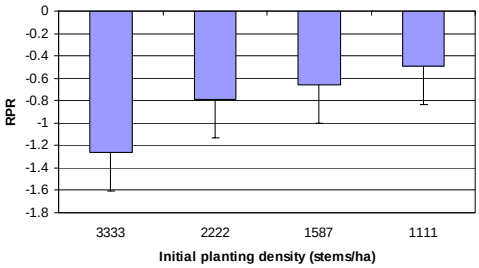


Figure 57: Mean RPR for plots at mean basal area of 0.009 m^2

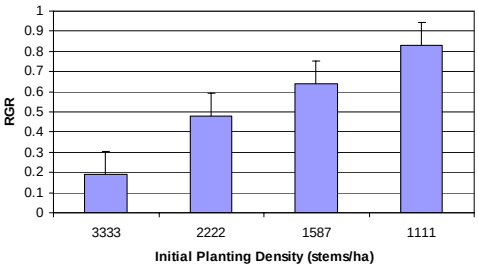


Figure 58: Mean RGR for plots at mean basal area of 0.009 m^2

Although the differences in RPR at 0.015 m^2 mean basal area, between planting densities are not significant, the inverse relationship between RPR and planting density remains (figure 59). The differences in RGR however are statistically significant (figure 60).

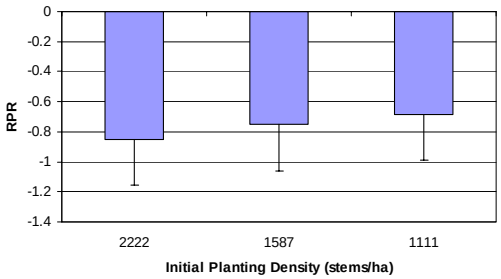


Figure 59: Mean RPR for plots at mean basal area of 0.015m^2

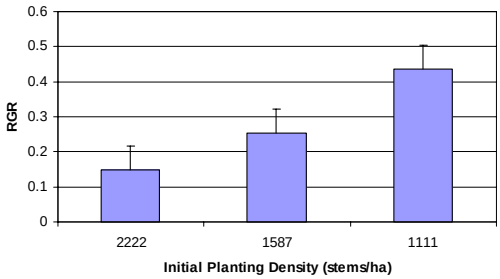


Figure 60: Mean RGR for plots at mean basal area of 0.015 m^2

These results indicate that hypothesis 1, which states “increased stand density results in increased competition between individuals within the stand”, can be accepted.

4.2.5.2. Hypothesis 2

Basal area and RPR per tree were compared at a mean basal area per plot of 0.007 m^2 and 0.009 m^2 (figures 61 and 62). It can be seen that smaller trees within plots with the same mean basal area have a lower RGR than larger trees.

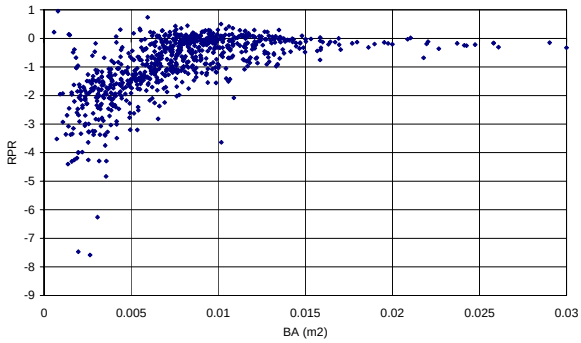


Figure 61: Relationship between basal area and RGR on an individual tree basis at a mean basal area per plot of 0.007 m^2

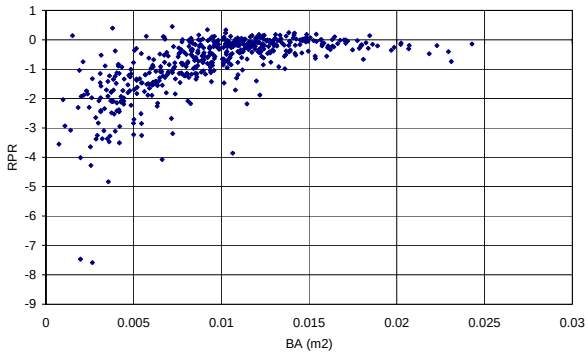


Figure 62: Relationship between basal area and RGR on an individual tree basis at a mean basal area per plot of 0.009 m^2

In order to quantify this relationship statistically, two size-classes were identified, namely: “dominant” and “the rest”. The three biggest trees per plot were categorised as dominant using logic similar to part of that used to define top height. In the South African forest industry, the concept of “top height” is widely accepted (Breedenkamp 1993). This involves the use of the 20% thickest trees per hectare together with age to define site index. The reasoning behind using the 20% thickest trees is that they are considered to be the dominant trees, and thought to be relatively independent of silviculture (of which initial planting density is a major component). In South Africa common practice is to use between 1111 stems.ha^{-1} and 1667 stems.ha^{-1} as the standard initial planting density. Twenty percent of 1667 stems.ha^{-1} and 1111 stems.ha^{-1} is equal to 333 stems.ha^{-1} and 222 stems.ha^{-1} respectively. For this reason it was decided to use the 300 largest trees per hectare to represent the dominant size class. The 300 largest trees per hectare equates to approximately 3 trees per plot. This is calculated as follows:

- Size of measured plots = 94.5 m^2 for the 1587 stems.ha-1 treatment
  = 81 m^2 for all the other plots

- Therefore the 3 biggest trees per plot represent the biggest 317 stems.ha^{-1} and 370 stems.ha^{-1} for the 94.5m^2 and 81m^2 plots respectively.

Those trees not categorised as dominant, fell into the “rest” category. The mean RPR and RGR of the dominant, and rest trees, was calculated per plot at a mean plot basal area of 0.007 m^2, 0.009 m^2 and 0.015 m^2. This was then analysed using analysis of variance.

Table 19: Results from ANOVA comparing the RGR and RPR of the dominant trees and the rest at 0.007 m^2, 0.009 m^2 and 0.015 m^2 mean basal area.

Mean Tree Basal Area	Variant	Factor	F pr.
0.007 m^2	RGR	Canopy Class	<0.001
0.009 m^2	RGR	Canopy Class	<0.001
0.015 m^2	RGR	Canopy Class	<0.001
0.007 m^2	RPR	Canopy Class	<0.001
0.009 m^2	RPR	Canopy Class	<0.001
0.015 m^2	RPR	Canopy Class	<0.001

The size-class, initial planting density and their interaction were all highly significant in explaining the variation in RPR at mean basal area per plot equal to 0.007 m^2, 0.009 m^2 and 0.015 m^2. The RPR and RGR of the dominant trees were statistically significantly greater than the rest of the trees (figures 63, 64, 65, 66, 67 an 68). Based on this result, hypothesis two which states "Larger trees use disproportionately more resources than smaller ones and therefore competition is asymmetrical" can be accepted.

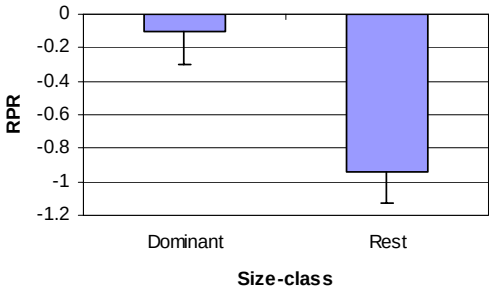


Figure 63: RPR of different size-classes at a mean basal area of 0.007 m^2

Figure 64: RGR of different size-classes at a mean basal area of 0.007 m^2

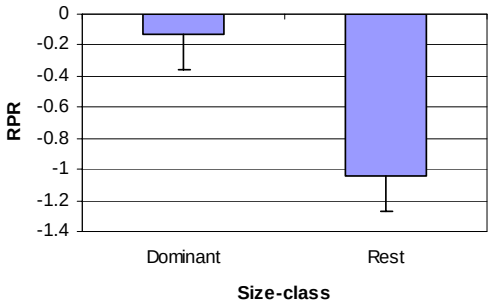


Figure 65: RPR of different size-classes at a mean basal area of 0.009 m^2

Figure 66: RGR of different size-classes at a mean basal area of 0.009 m^2

Figure 67: RPR of different size-classes at a mean basal area of 0.015m^2

Figure 68: RGR of different size-classes at a mean basal area of 0.015 m^2

Both RGR and RPR in decreased as mean basal area per plot increased.

4.2.5.3. Hypothesis 3 and 4

The mean basal area of the three biggest trees per plot was modelled through time, using non-linear regression to estimate the coefficients for the Gompertz function (see appendix 5). One hundred percent of the variance was accounted for with a standard error of observations estimated to be 0.000118. The resulting model was then used to derive the ages at which the mean dominant basal area per plot was 0.013 m^2 and 0.22 m^2, respectively. This age was then inserted into the individual trees model, and the biggest three trees per plot extracted.

The mean RPR and RGR of the three biggest trees per plot at mean basal areas of 0.013 m^2 and 0.022 m^2 respectively were analysed.

Table 20: Table of results of ANOVA for RPR and RGR of dominant trees

Mean Basal area of Dominant trees	Measure of vigour	Planting Density	Genotype	Planting Density x Genotype
0.013 m^2	RPR	0.399	0.004	0.357
	RGR	<0.001	<0.001	0.285
0.022 m^2	RPR	0.287	0.003	0.281
	RGR	<0.001	<0.001	0.436

From table 20 it can be seen that planting density is highly significant in explaining the variation in RGR at both mean dominant basal areas. However, planting density is not significant in explaining the variation in RPR at either mean dominant basal area. RGR of the dominant trees at a fixed mean dominant basal area is inversely correlated to planting density (figures 70 and 72). If RGR is accepted as the measure of vigour to be used then hypothesis 3 which states, “when trees in a stand are competing for resources, smaller competitors take up some of the resources required by the larger ones, thereby slowing their growth, therefore competition is two-sided”, can be accepted. If RPR is the only measure of vigour, which is acceptable, then hypothesis 3 has to be rejected, as there is no statistically significant interaction between RPR and planting density at either mean dominant basal area (figures 69 and 71). If hypothesis 3 is rejected, then hypothesis must be rejected, as one of the pre-requisites of accepting hypothesis 4 is the acceptance of hypothesis 3.

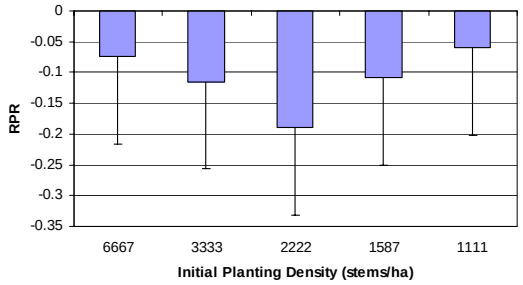


Figure 69: RPR of dominant trees at a mean dominant basal area of 0.013m^2

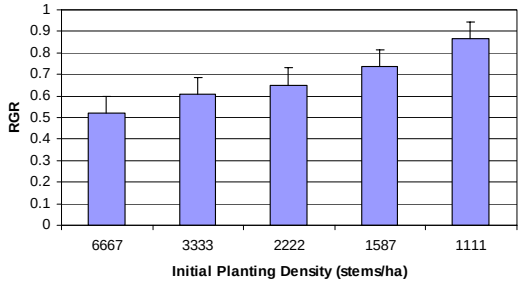


Figure 70: RGR of dominant trees at a a mean dominant basal area of 0.013 m^2

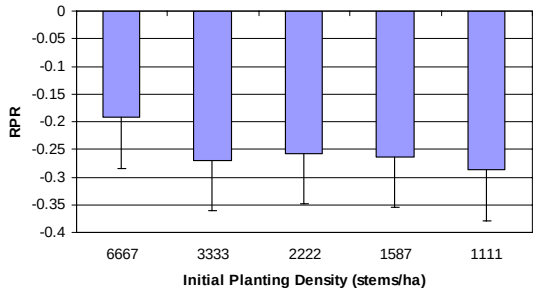


Figure 71: RPR of dominant trees at a mean dominant basal area of 0.022m^2

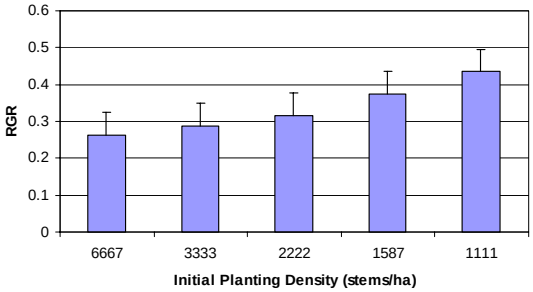


Figure 72: RGR of dominant trees at a a mean dominant basal area of 0.022 m^2

There is no interaction between genotype and planting density for RPR or RGR at either mean dominant basal area (table 20). Therefore hypothesis 4, which states, “suppressed trees in the clonal treatments reduce the growth of larger competitors to a greater extent than do the suppressed trees in the seedling treatments”, cannot be accepted. If this hypothesis were to have been accepted then a trend of increasing difference between clonal and seedling treatments for RPR an RGR with increasing planting density would have been expected. This was not the case (figure 73-76).

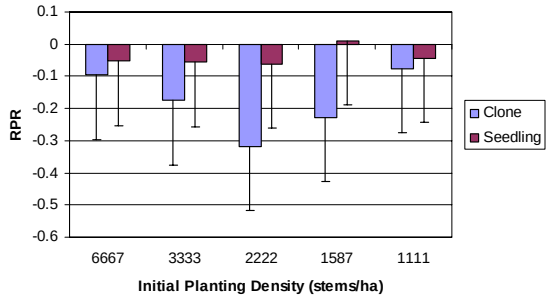


Figure 73: RPR of dominant trees at a mean dominant basal area of 0.013m^2

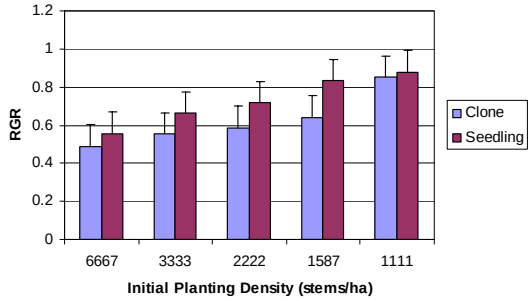


Figure 74: RGR of dominant trees at a a mean dominant basal area of 0.013 m^2

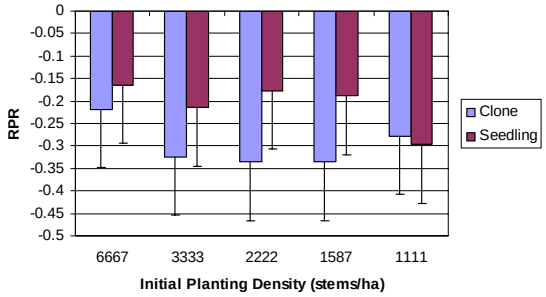


Figure 75: RPR of dominant trees at a mean dominant basal area of 0.022m^2

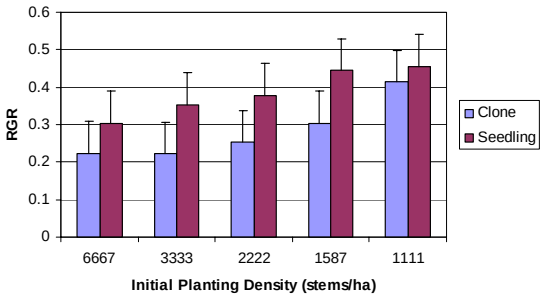


Figure 76: RGR of dominant trees at a a mean dominant basal area of 0.022 m^2

4.2.6. Modelling skewness and CV% of plots at equal mean tree size.

Skewness as well as the coefficient of variation (CV%) was calculated for each plot at that point in time where the mean basal area per tree within that plot was equal to 0.007 m^2 and 0.009 m^2 respectively. At 0.009 m^2 mean basal area, the 6667 stems.ha^{-1} treatments could not be included in the analysis because the 6667 stems.ha^{-1} clonal treatments did not reach 0.009m^2 mean basal area within the study period.

Table 21: Table of results of ANOVA for CV% and skewness at 0.007 m2 and 0.009 m2 mean basal area.

Mean Basal area per plot	Measure	Planting Density	Genotype	Planting Density x Genotype
0.007 m^2	CV%	<0.001	0.029	0.114
	Skewness	<0.001	0.409	0.010
0.009 m^2	CV%	<0.001	0.125	0.847
	Skewness	<0.001	0.059	0.067

At 0.007 m^2 mean basal area, the CV% in clonal treatments was statistically greater than in seedling treatments. The CV% in clonal treatments at 0.009m^2 was also higher than the seedling treatments, however this difference was not statistically significant. Planting density was highly significant in explaining the variation in basal area at 0.007 m^2 and 0.009 m^2 mean basal area (table 21).

At 0.007 m^2 mean basal area, the 6667 stems.ha^{-1} planting density in the seedling and clonal treatments, had a significantly higher degree of variation than the 3333 stems.ha^{-1} plots, which in turn had a significantly higher degree of variation than all the other treatments. The only statistically significant difference in variation between genotypes at the same mean basal area and same planting density occurred in the 6667 stems.ha^{-1} treatment, where the variation in the clonal treatment was significantly higher than in the seedling treatments (figure 77).

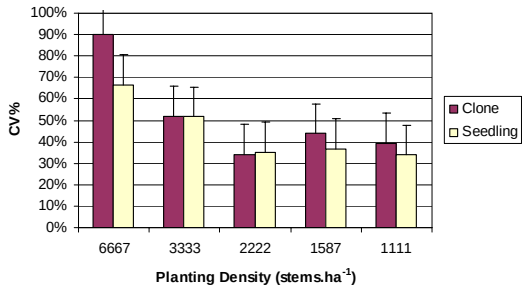


Figure 77: CV% of different treatments tested at a mean basal area per plot of 0.007 m2

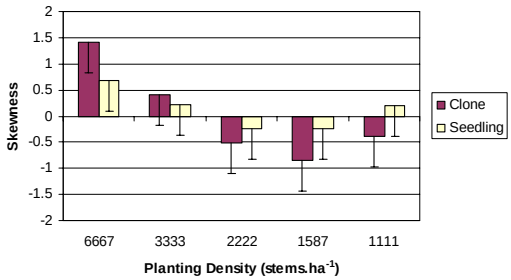


Figure 78: Skewness of different treatments tested at a mean basal area per plot of 0.007 m2

At 0.009m^2, the highest planting density treatment (3333 stems.ha^{-1}) had a statistically significantly higher degree of variation between trees than did any of the other planting density treatments (figure 79). Within planting density treatments there was no significant difference in CV% between genotypes (figure 79). At both mean basal areas, there was a trend for CV% to increase with planting density, once some critical planting density for that mean basal area was exceeded.

At 0.007 m^2 and 0.009 m^2 mean basal area, planting density was found to be highly significant in explaining the variation in population skewness (table 21). There was a trend for skewness to increase (shift from negative to positive) with an increase in planting density. This tendency is more evident in the clonal treatments, which are more sensitive to planting density in terms of skewness. At 0.007m^2 basal area only the 6667 stems.ha^{-1} seedling treatment is significantly different from the rest of the seedling treatments in terms of skewness. However at 0.009m^2 there is no difference in skewness between seedling planting density treatments (figure 80).

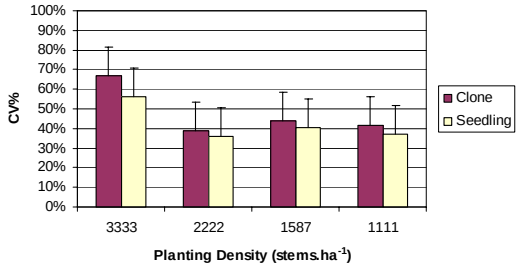


Figure 79: CV% of different treatments tested at a mean basal area per plot of 0.009 m2

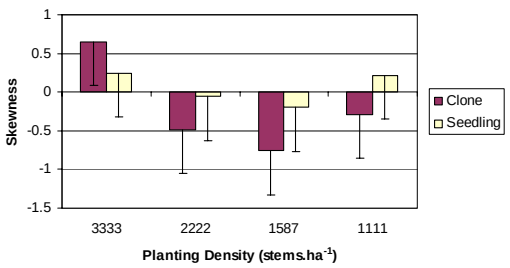


Figure 80: Skewness of different treatments tested at a mean basal area per plot of 0.009 m2

4.3. Physiological characteristics of the population

4.3.1. Development of allometric relationships

Allometric relationships were developed for the calculation of (i) specific leaf area (SLA), (ii) leaf area, (iii) stem mass, (iv) bark mass, (v) live branch mass, (vi) stem wood density and (vii) full-tree volume, using DBH as a surrogate. These relationships were developed through the use regression.

A separate relationship was developed for each genotype at each sampling event. A power function was found to best describe the relationship between DBH and SLA, DBH and leaf area, DBH and stem mass as well as DBH and bark mass. An exponential function was found to best describe the relationship between DBH and live branch mass. A linear model utilising the natural logarithm of DBH as the independent variable best described the relationship between DBH and stem wood density. A third degree polynomial function with no constant best described the relationship between DBH and full tree volume.

The derived coefficients, as well as goodness of fit statistics for these relationships have been presented in table 22.

Table 22: Allometric relationships generated to calculate stand level biomass production and partitioning

Biomass Component	Sampling Year	Genotype	b_0	b_1	R^2	n	Comment
Model = b_0 x DBH^{b1}							
SLA	1999	Clone	15.405	-0.1036	3.1%	19	No relationship
SLA	1999	Seedling	22.913	-0.3351	29.5%	20	No relationship
SLA	2002	Clone	49.237	-0.5336	76.7%	20	Good fit
SLA	2002	Seedling	48.088	-0.6048	56.7%	20	Acceptable fit
Leaf Area	1999	Clone	0.004	3.5719	95.3%	17	Excellent fit
Leaf Area	1999	Seedling	0.0036	3.6625	91.0%	20	Excellent fit
Leaf Area	2002	Clone	0.1246	1.9487	92.3%	19	Excellent fit
Leaf Area	2002	Seedling	0.0307	2.3514	72.0%	19	Good fit
Leaf Mass	1999	Clone	0.0002	3.8896	92.4%	18	Excellent fit
Leaf Mass	1999	Seedling	0.0002	3.907	94.4%	20	Excellent fit
Leaf Mass	2002	Clone	0.0024	2.5051	96.0%	19	Excellent fit
Leaf Mass	2002	Seedling	0.0007	2.9497	80.2%	19	Good fit
Stem Mass	1999	Clone	0.1381	2.1009	96.6%	18	Excellent fit
Stem Mass	1999	Seedling	0.1238	2.1398	97.6%	20	Excellent fit
Stem Mass	2002	Clone	0.0365	2.7199	98.5%	18	Excellent fit
Stem Mass	2002	Seedling	0.0612	2.531	96.7%	20	Excellent fit
Bark Mass	1999	Clone	0.006	2.4354	81.3%	18	Good fit
Bark Mass	1999	Seedling	0.0092	2.3532	95.1%	19	Excellent fit
Bark Mass	2002	Clone	0.0033	2.6746	96.7%	19	Excellent fit
Bark Mass	2002	Seedling	0.0183	2.1486	95.2%	20	Excellent fit
Model = b_o x exp(b_1 x DBH)							

Live Branch Mass	1999	Clone	0.1195	0.3361	89.5%	18	Excellent fit
Live Branch Mass	1999	Seedling	0.1159	0.3048	96.2%	20	Excellent fit
Live Branch Mass	2002	Clone	0.4276	0.1609	91.7%	19	Excellent fit
Live Branch Mass	2002	Seedling	0.2443	0.1721	84.9%	19	Good fit
Model = b0 + b1 ln(DBH)							
Stem Wood Density	1999	Clone	0.4394	-0.0115	0.6%	18	No relationship
Stem Wood Density	1999	Seedling	0.3343	0.0274	4.3%	20	No relationship
Stem Wood Density	2002	Clone	-0.0842	0.1677	73.7%	17	Good fit
Stem Wood Density	2002	Seedling	0.0817	0.1044	52.6%	20	Acceptable fit

Model = b_1x DBH + b_2 x DBH^2 + b_3 x DBH^3

Biomass Component	Sampling Year	Genotype	b_1	b_2	b_3	R^2	n	Comment
Full-Tree Volume	1999	Clone	-0.0027	0.0009	-0.00002	98.9%	17	Excellent fit
Full-Tree Volume	1999	Seedling	-0.0026	0.0009	-0.00002	97.7%	20	Excellent fit
Full-Tree Volume	2002	Clone	-0.0098	0.0021	-0.00004	98.4%	18	Excellent fit
Full-Tree Volume	2002	Seedling	-0.0126	0.0023	-0.00004	98.4%	20	Excellent fit

4.3.2. Production

Allometric equations developed in section 4.3.1, with DBH as the independent variable, were used to calculate the production per hectare of each biomass fraction. This was done by calculating the dry mass of each biomass fraction for each tree in the experiment using these allometric relationships. These dry masses were then summed per plot and extrapolated to a per hectare value at each destructive sampling event.

4.3.2.1. Specific leaf area (SLA)

Using the relationship developed between DBH and SLA it was possible to obtain a treatment value for SLA, which was weighted in terms of the DBH distribution in each treatment. This could only be done for the destructive sampling exercise carried out at age 5.5 years as no relationship between DBH and SLA could be established in the 2002 biomass sampling exercise.

Table 23: Results from ANOVA for SLA at age 5.5

Factor	F pr.
Planting Density	>0.001
Genotype	>0.001
Planting Density x Genotype	>0.001

From figure 81 it is clear that the SLA of the clone is significantly higher than that of the seedling ($p<0.001$ at the 5% level). Planting density was highly significant ($p<0.001$ at the 5% level) in explaining the variation in SLA. The interaction between genotype and planting density was also highly significant ($p<0.001$ at the 5% level) in explaining the variation in SLA. The rate at which SLA increased with an increase in planting density was greater in the clone

than in the seedling (figure 81). Therefore the seedling was more sensitive to an increase in planting density.

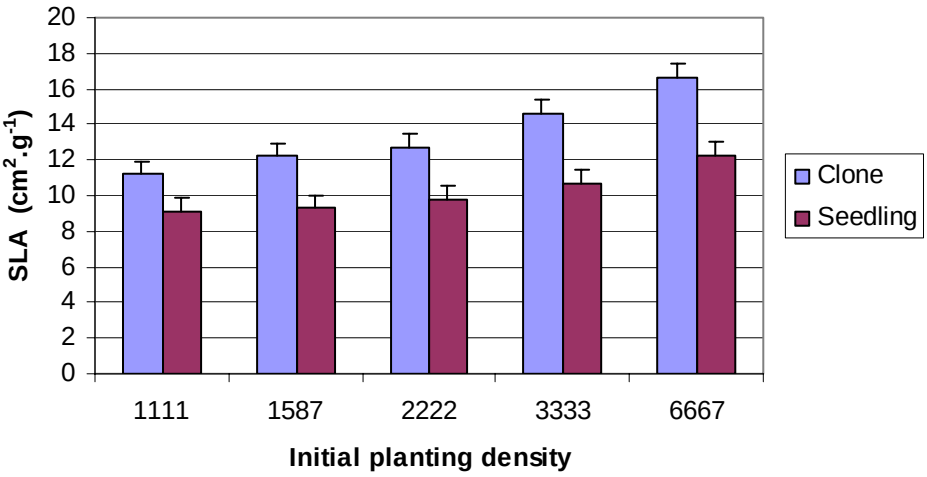


Figure 81: Mean specific leaf area at stand level for all treatments at age 5.5 years

4.3.2.2. Leaf area

Using separate allometric relationships (table 22) developed at each destructive sampling event, leaf area per ha was calculated from individual trees within each plot. The leaf area per hectare at each sampling event was analysed to understand how much of the variation was explained by planting density, genotype or their interaction.

Table 24: Results of ANOVA for leaf area per hectare

Sampling year	Factor	F pr.
1999	Planting Density	<0.001
	Genotype	<0.001
	Planting Density x Genotype	0.006
2002	Planting Density	<0.001
	Genotype	<0.001
	Planting Density x Genotype	<0.001

Leaf area was higher at age 2.5 years than at age 5.5 years. The difference between sampling events was 4087 m^2. This difference was as a result in a mean increase of 3714 m^2 in the clone, and more significantly a mean decrease of 11415 m^2 in the seedling treatments.

At age 2.5 years (1999) the seedling treatments were producing significantly more leaf area per hectare (figure 82) than the clonal treatments. By age 5.5 years (2002) the clonal treatments were producing significantly more leaf area than the seedling treatments (figure 83).

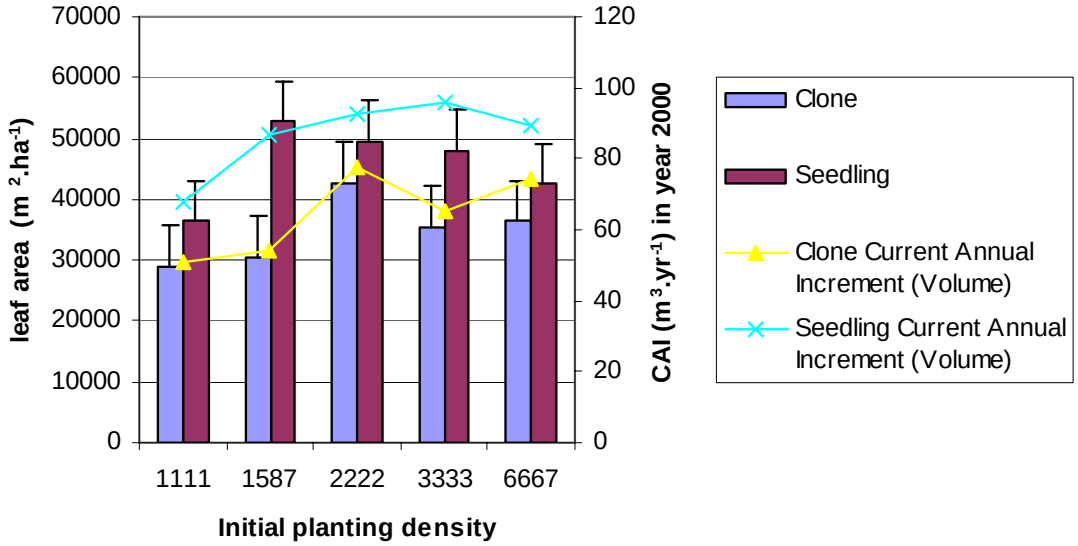


Figure 82: Leaf area at stand level for all treatments at age 2.5 years

At age 2.5 years (1999), with the exception of the 1111 stems.ha^{-1} treatment, there was a trend in the seedling treatments for leaf area per hectare to increase with a reduction in planting density. In the literature it has been reported that leaf area per hectare is closely correlated with CAI (volume) in the following year. When leaf area at age 2.5 years (1999) was compared to CAI for full tree volume at age 3.5 years (2000), there was a high level of coincidence (figure 82).

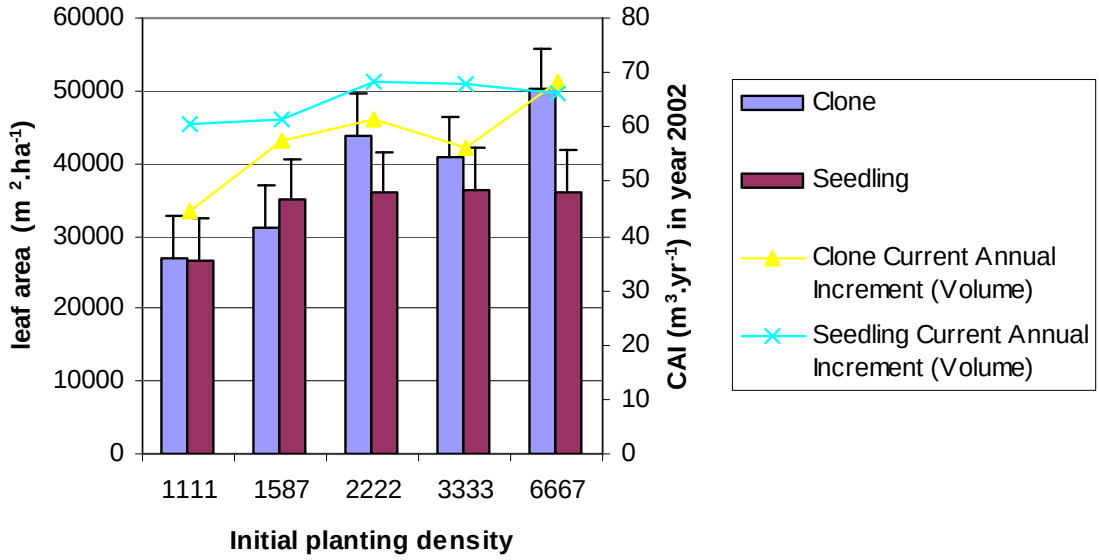


Figure 83: Leaf area at stand level for all treatments at age 5.5 years

At age 5.5 years there was no statistically significant difference in leaf area between the 1587 stems.ha^{-1}, 2222 stems.ha^{-1}, 3333 stems.ha^{-1} and 6667 stems.ha^{-1} seedling treatments. The leaf area per hectare for the 1111 stems.ha^{-1} seedling treatment was statistically significantly less than all the other seedling treatments. There was a trend for leaf area per hectare to

increase with increasing planting density. This trend was particularly evident in the clonal treatments. The leaf area per hectare could not be compared to CAI at age 6.5 years, as this was past the end of the study period. There was however, a very high degree of coincidence between leaf area per hectare at age 5.5 years (2002) and CAI for full tree volume at age 5.5 years (see figure 83).

4.3.2.3. Leaf mass

The leaf mass per hectare of the seedling was statistically significantly greater than the clone at both sampling events. As with leaf area per hectare, planting density, genotype explained a statistically significant portion of the variation in leaf mass per hectare at both sampling events. The interaction between planting density and genotype explained a statistically significant portion of the variation in leaf mass per hectare.

Table 25: Results of ANOVA for leaf mass per hectare

Sampling year	Factor	F pr.
1999	Planting Density	<0.001
	Genotype	<0.001
	Planting Density x Genotype	0.006
2002	Planting Density	0.005
	Genotype	<0.001
	Planting Density x Genotype	0.061

As with leaf area, there was an overall reduction in leaf mass from age 2.5 years to age 5.5 years. However, unlike leaf area this reduction was as a result of reduced leaf mass per hectare in both seedling and clonal treatments.

The decrease in leaf area in seedling treatments, between sampling events, can therefore be explained by a decrease in leaf mass per hectare. The slight increase in leaf area per hectare in the clonal treatments, can however not be explained by a decrease in leaf mass per hectare. It must therefore be concluded that the increase in leaf area per hectare in the clonal treatments between sampling events, was as a result of an increase in SLA.

At age 2.5 years there was no statistically significant difference in leaf mass per hectare for all the clonal planting density treatments, with the exception of the 2222 stems.ha^{-1} treatment, which had significantly more leaf mass than the rest (figure 84). With the exception of the 1111 stems.ha^{-1} treatment, the leaf mass per hectare of all seedling treatments at age 2.5 years, decreased with an increase in planting density. The 1111 stems.ha^{-1} seedling treatment was the least productive seedling treatment in terms of planting density (figure 84).

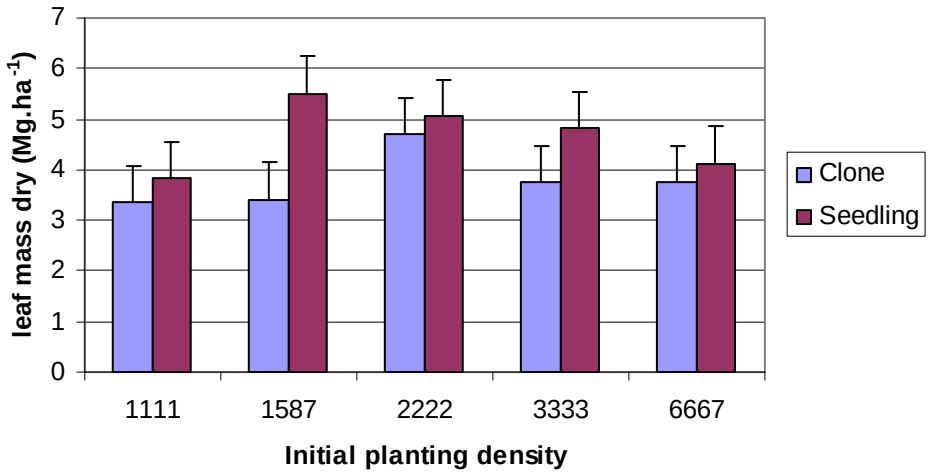


Figure 84: Leaf mass at stand level for all treatments at age 2.5 years

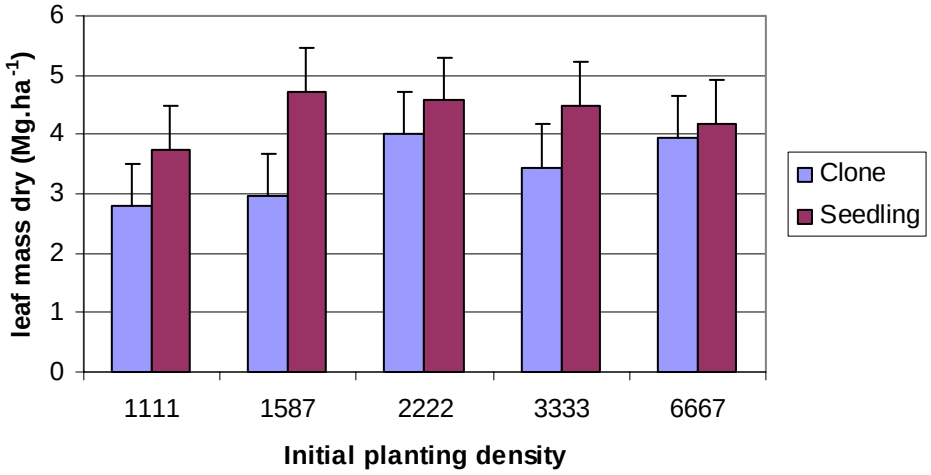


Figure 85: Leaf mass at stand level for all treatments at age 5.5 years

4.3.2.4. Branch Mass

At both sampling events the clonal treatments were producing statistically significantly more branch material than the seedling treatments (F pr >0.001). There was an overall increase in branch mass from 7921 mega grams (Mg) per hectare to 8214 $Mg.ha^{-1}$ between ages 2.5 years and 5.5 years.

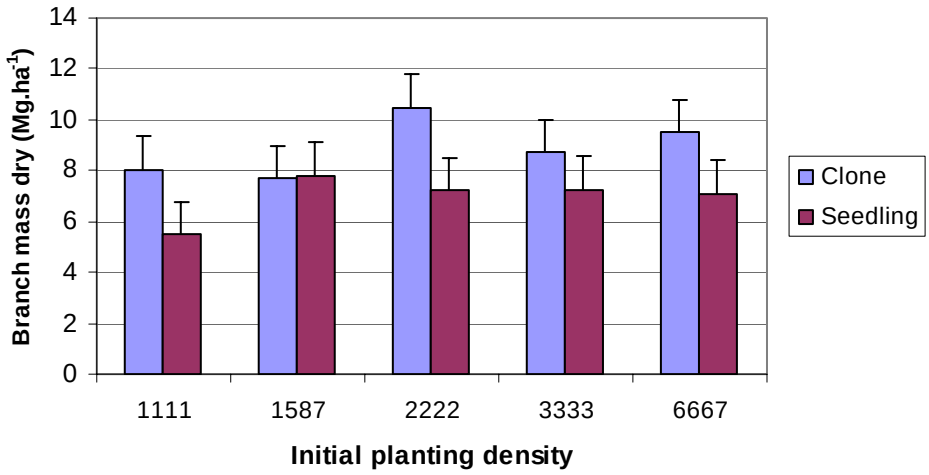


Figure 86: Live-branch mass at stand level for all treatments at age 2.5 years

At age 2.5 years there was no statistically significant difference in the seedling live branch mass, between the 1587 stems.ha^{-1}, 2222 stems.ha^{-1}, 3333 stems.ha^{-1} and 6667 stems.ha^{-1} treatments. The 1111 stems.ha^{-1} seedling treatment did however produce less branch mass per hectare that the other seedling treatments. There was however a slight trend for live branch mass per hectare to increase with a decrease in planting density in the seedling treatments (figure 86).

At age 2.5 years the 2222 stems.ha^{-1} clonal treatment had statistically significantly greater live branch mass than all other clonal treatments other than the 6667 stems.ha^{-1} treatment.

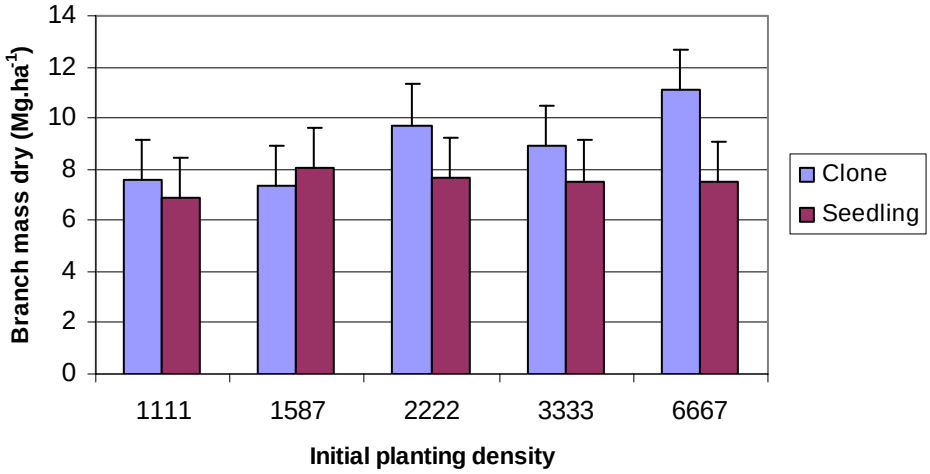


Figure 87: Live-branch mass at stand level for all treatments at age 5.5 years

At age 5.5 years there was no significant difference in live branch mass per hectare between seedling planting density treatments. There was a trend for live branch mass per hectare to increase with planting density in the clonal treatments at age 5.5 years (figure 87).

4.3.2.5. Dry Stem Mass

Table 26: Results of ANOVA for dry stem mass per hectare

Sampling year	Factor	F pr.
1999	Planting Density	<0.001
	Genotype	0.002
	Planting Density x Genotype	0.019
2002	Planting Density	<0.001
	Genotype	<0.001
	Planting Density x Genotype	0.165

At age 2.5 years the seedling produced statistically significantly more volume than the clone. The only significant difference between treatments occurred in the 1587 stems.ha^{-1} treatments, where the seedling produced more volume than the clone. Planting density was highly significant in explaining the variation in dry stem mass per hectare (table 26). An increase in planting density resulted in an increase in stem mass.

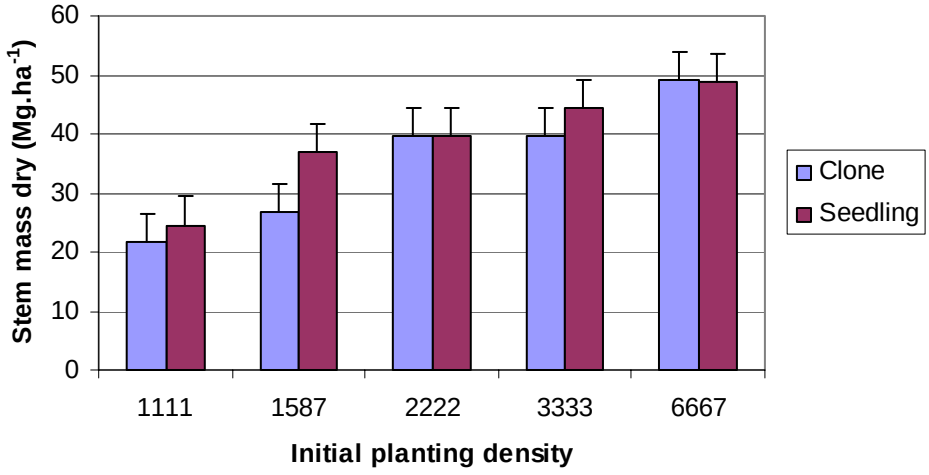


Figure 88: Stem mass at stand level for all treatments at age 2.5 years

At age 5.5 years the seedling had produced significantly more stems mass per hectare than the clone. Even though not always statistically significant the seedling out produced the clone in all planting density treatments (figure 89). There was no significant difference between the 1587 stems.ha^{-1}, 2222 stems.ha^{-1}, 3333 stems.ha^{-1} and 6667 stems.ha^{-1} seedling treatments. The 1111 stems.ha^{-1} seedling treatments produced significantly less volume than the other seedling treatments.

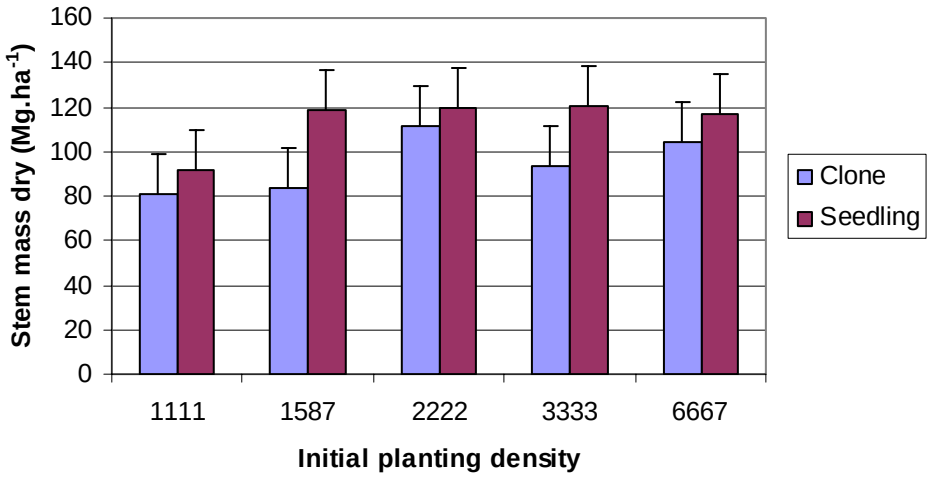


Figure 89: Stem mass at stand level for all treatments at age 5.5 years

4.3.2.6. Bark mass

The seedling produced significantly more bark per hectare than the clone at both sampling events. At both sampling events bark mass production tended to increase with an increase in planting density, however this trend was more evident at age 2.5. At age 2.5 years the seedling treatments produced significantly more bark per hectare than the clone in every planting density treatment (figure 90).

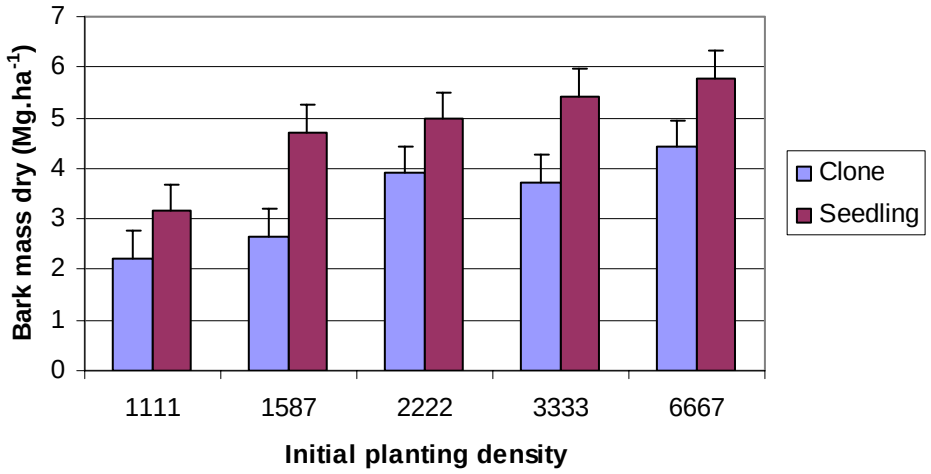


Figure 90: Bark mass at stand level for all treatments at age 2.5 years

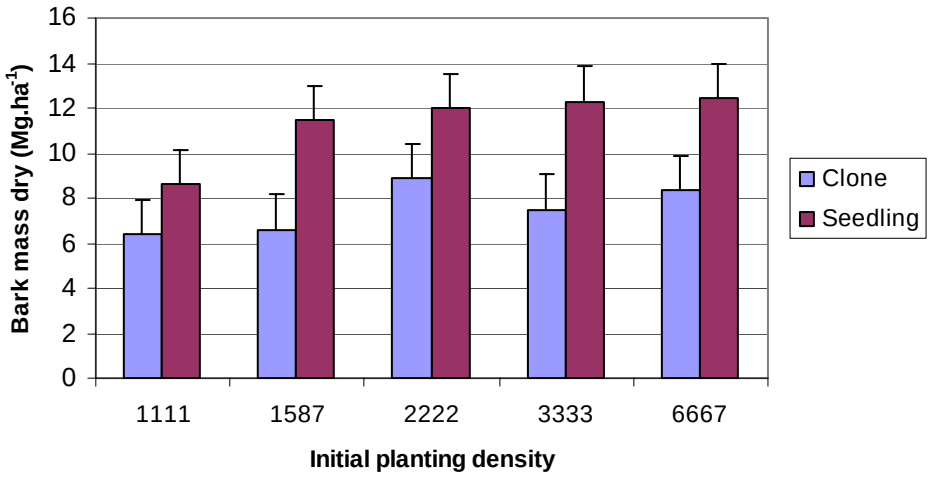


Figure 91: Bark mass at stand level for all treatments at age 5.5 years

4.3.2.7. Total Biomass

Total biomass (dry) increased from one sampling event to the next. The seedling produced significantly more biomass than the clone at both sampling events. This difference between genotypes increased from 3.9 $Mg.ha^{-1}$ to 21.7 $Mg.ha^{-1}$ between sampling events.

Table 27: Results of ANOVA for total biomass per hectare

Sampling year	Factor	F pr.
1999	Planting Density	<0.001
	Genotype	0.018
	Planting Density x Genotype	0.014
2002	Planting Density	<0.001
	Genotype	<0.001
	Planting Density x Genotype	0.162

At the 1999 sampling event, total biomass production per hectare was found to have increased progressively with an increase in planting density. With the exception of the 1587 $stems.ha^{-1}$ treatment there was no significant difference between genotypes at any of the other planting density treatments (figure 92).

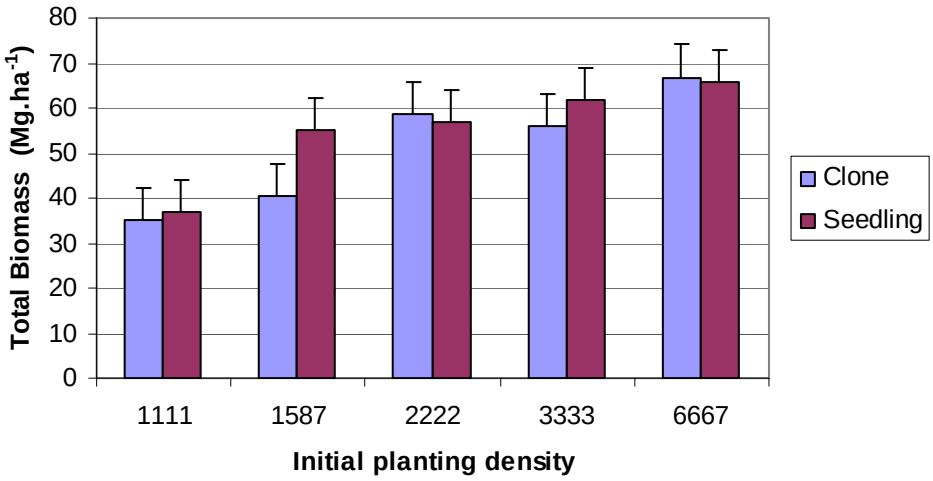


Figure 92: Total biomass at stand level for all treatments at age 2.5 years

At the 2002 sampling event the 1111 stems.ha^{-1} seedling treatment had produced significantly less biomass than all the other seedling treatments, which where not statistically different from one another (figure 93). Even though not statistically significant, at each planting density treatment the seedling produced more biomass per hectare than the clone (figure 93).

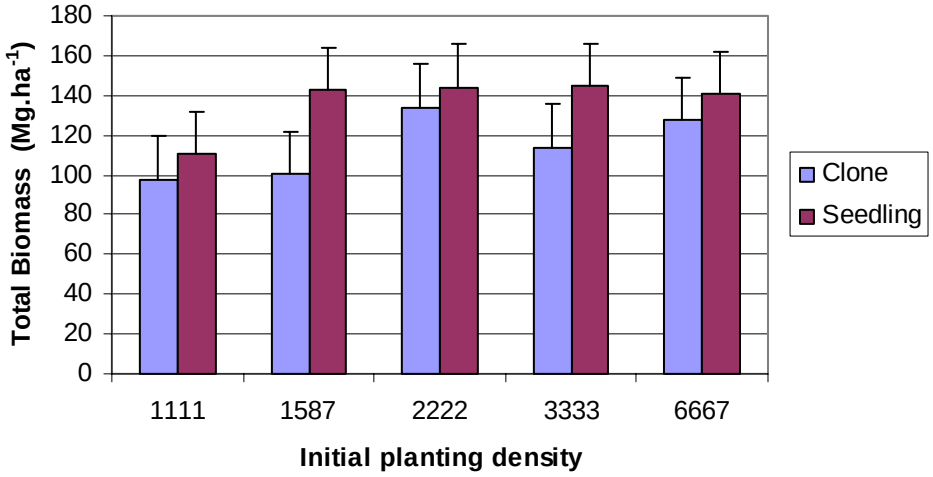


Figure 93: Total biomass at stand level for all treatments at age 5.5 years

4.3.2.8. Stem Wood Density

No allometric relationship could be established between DBH and stem wood density at the 1999 destructive sampling event. Therefore analysis could only be performed on the effect of genotype and planting density on stem wood density at the second sampling event (age 5.5).

Planting density, genotype and their interaction were all found to be highly significant (F pr < 0.001) in explaining the variation in mean stem wood density at age 5.5 years (table 28).

Table 28: Results of ANOVA for mean stem wood density

Sampling year	Factor	F pr.
2002	Planting Density	<0.001
	Genotype	<0.001
	Planting Density x Genotype	<0.001

Mean stem wood density decreased with an increase in planting density. This tendency was more pronounced in the clonal treatments (figure 94). This increased sensitivity of mean stem wood density to planting density is as a result of the steeper gradient in the allometric equation for the clonal treatments (table 22), as well as the higher number of smaller DBHs (therefore lower density) in the clonal treatments with higher planting densities (figure 17).

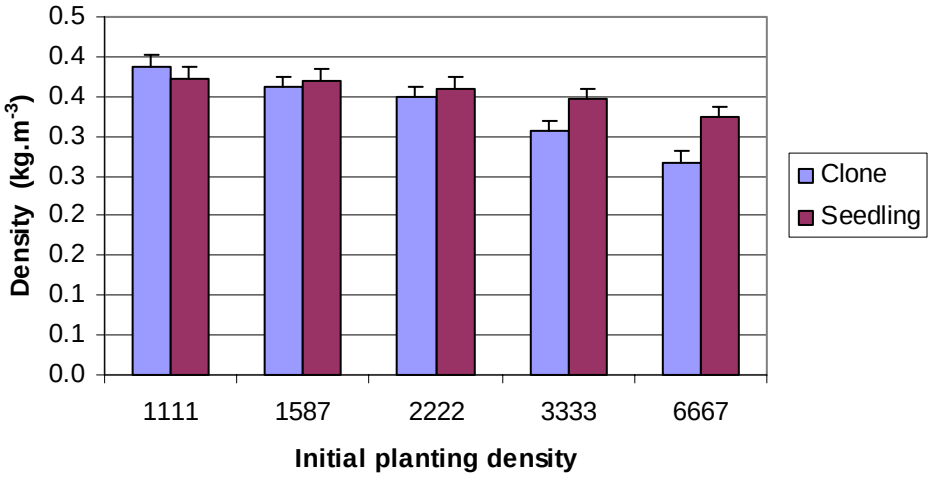


Figure 94: Mean stem wood density for all treatments at age 5.5 years

4.3.3. Biomass Partitioning

Biomass partitioning is quantified by means of percentages. All percentages have been transformed using the angular transformation to normalise the population: (Gomez and Gomez 1984):

$$Transformation = \frac{180}{\pi} * \text{arc\_sine}\sqrt{\frac{\%}{100}} \qquad \text{[Equation 30]}$$

All analyses were based on transformed values, however for interpretation purposes, all graphs have been represented using the untransformed values. Because untransformed values are used in the graphs, least significant differences cannot be represented on graphs as error bars, therefore letters of the alphabet have been used instead.

4.3.3.1. Leaf

The allocation of total biomass per hectare to leaves decreased from 8.15% in 1999 to 3.08% in 2002. At age 2.5 years in both the clonal and seedling treatments, the proportion of total biomass apportioned to leaves decreased with an increase in planting density.

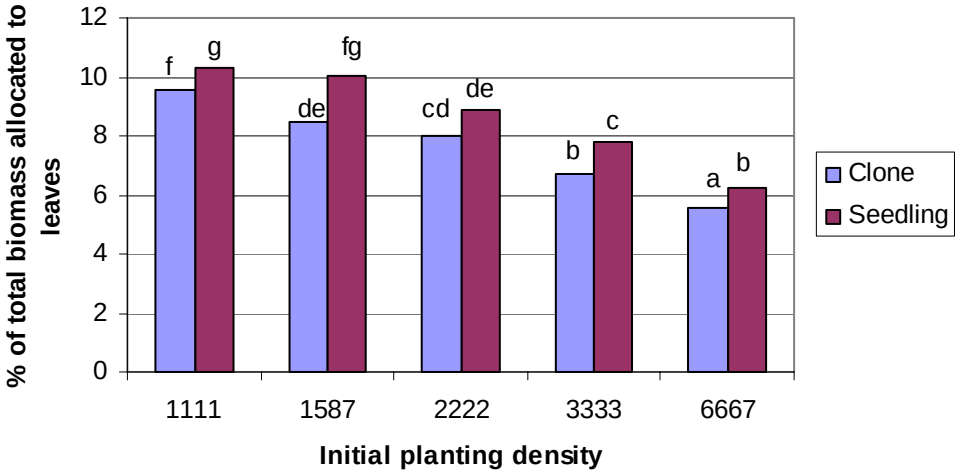


Figure 95: Percentage of total biomass allocated to leaves in 1999

At age 5.5 years biomass allocation to leaves in the seedling treatments also decreased with an increase in planting density. Conversely there was a very slight increase in allocation of biomass to leaves with an increase in planting density.

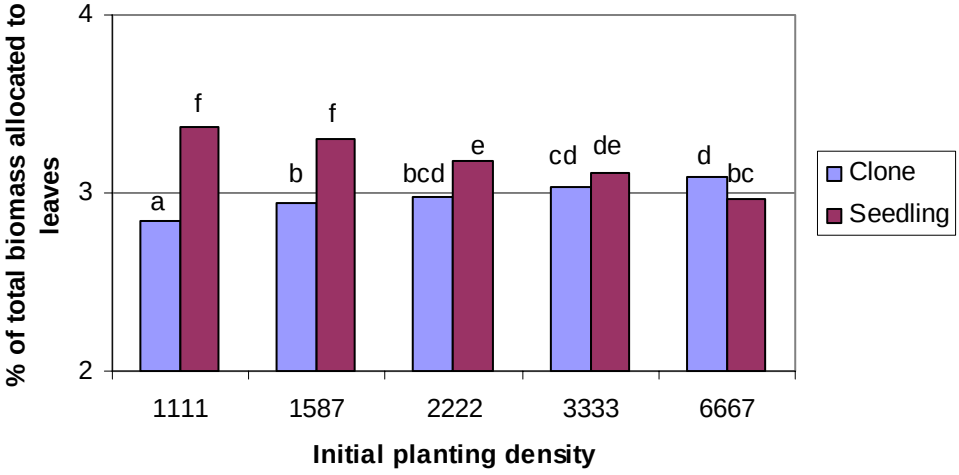


Figure 96: Percentage of total biomass allocated to leaves in 2002

4.3.3.2. Bark

At both destructive sampling events the seedling allocated more biomass to bark than did the clone. Allocation of biomass to bark increased with planting density in the seedling in both 1999 and 2002. Biomass allocation to bark was not affected by planting density in the clonal treatments, at either sampling event.

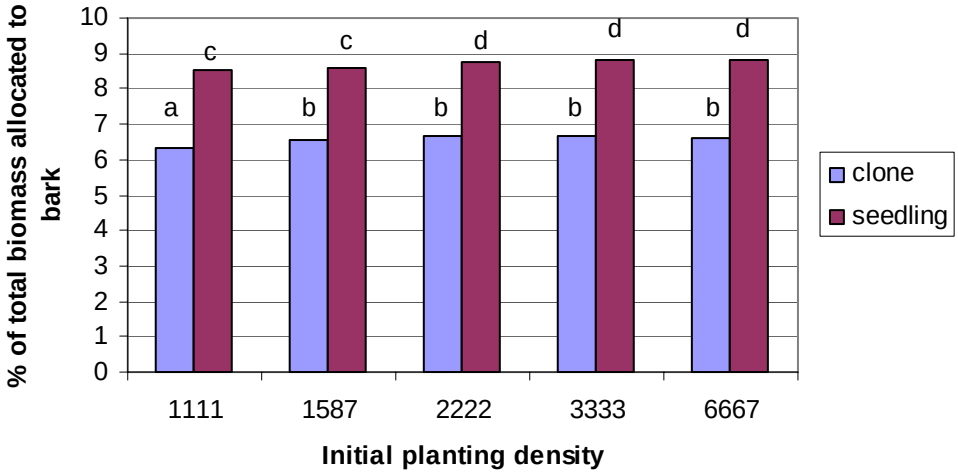


Figure 97: Percentage of total biomass allocated to bark in 1999

There was a small yet statistically significant decrease in proportional allocation of biomass to bark from 1999 to 2002.

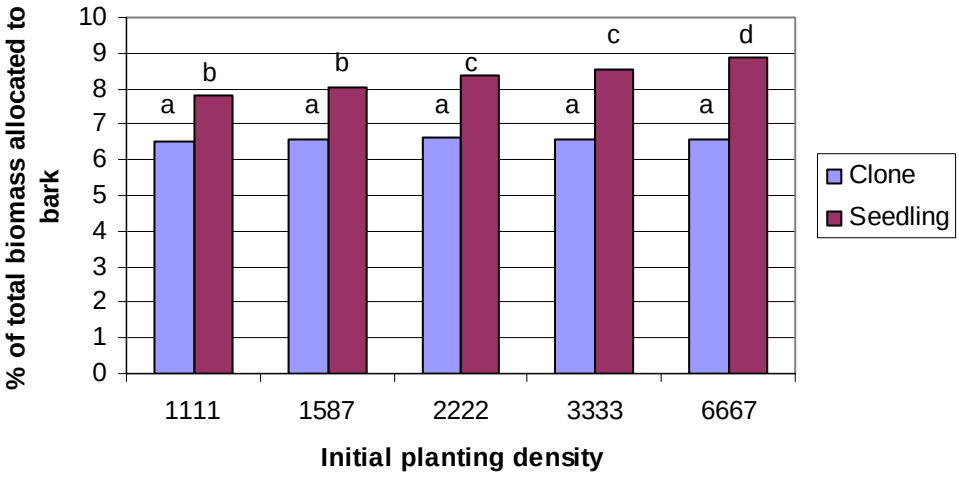


Figure 98: Percentage of total biomass allocated to bark in 2002

4.3.3.3. Branch

Percentage allocation of total biomass to live branches decreased from 1999 to 2002. The clone allocated a significantly larger proportion of its total biomass to branches than did the seedling at both sampling events (figures 99 and 100). At age 2.5 years both the seedling and clonal treatments experienced a reduction in percentage allocation of biomass to branches with an increase in planting density. The clonal treatments were more sensitive to planting density than the seedling treatments, in terms of proportional allocation of biomass to branches (figure 99).

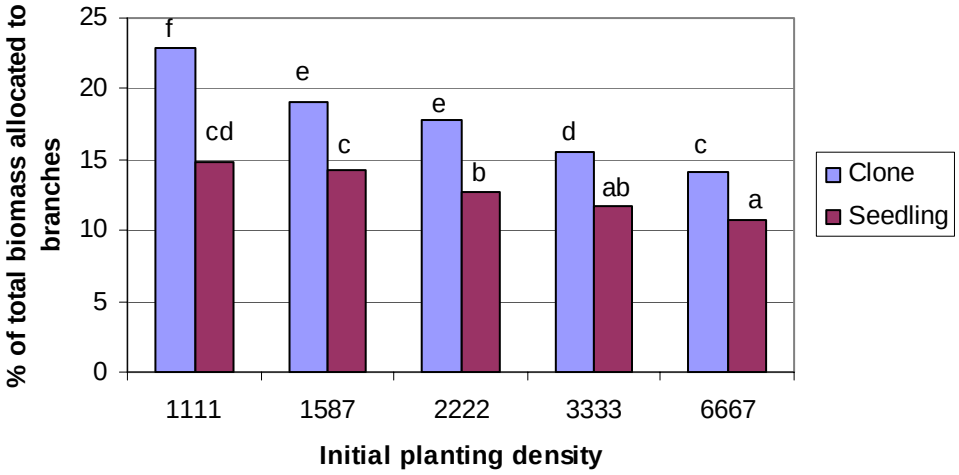


Figure 99: Percentage of total biomass allocated to live branches in 1999

At age 5.5 years, percentage allocation of total biomass to branches decreased with an increase in planting density (figure 100).

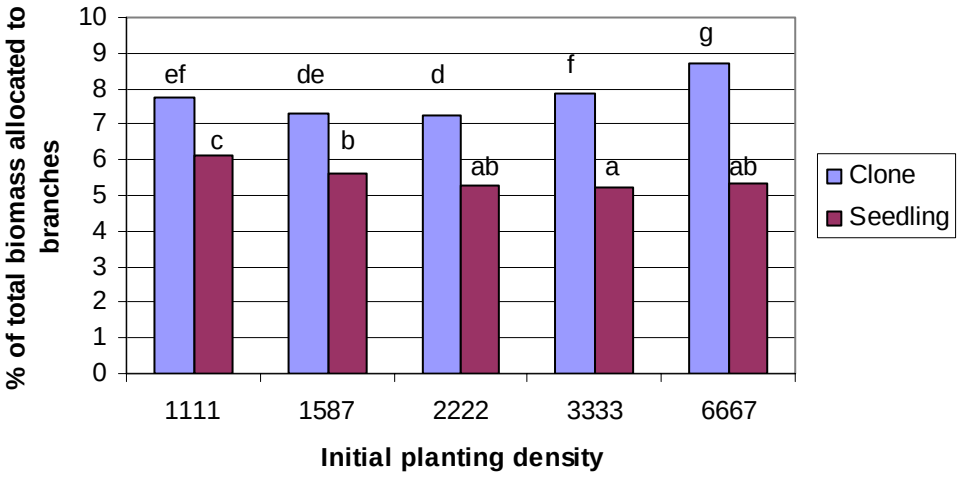


Figure 100: Percentage of total biomass allocated to live branches in 2002

4.3.3.4. Stem

Percentage allocation of total biomass to stem wood increased from 1999 to 2002. This was to be expected, as stem-wood is a permanent feature of biomass production and accrues with time, whereas other biomass fractions fall from the tree and are replaced with time. At 2.5 years there was a trend for a larger proportion of the total biomass per hectare, to be located in the stem wood of trees planted closer together than in those planted further apart (figure 101). This trend was stronger in the clone than in the seedling.

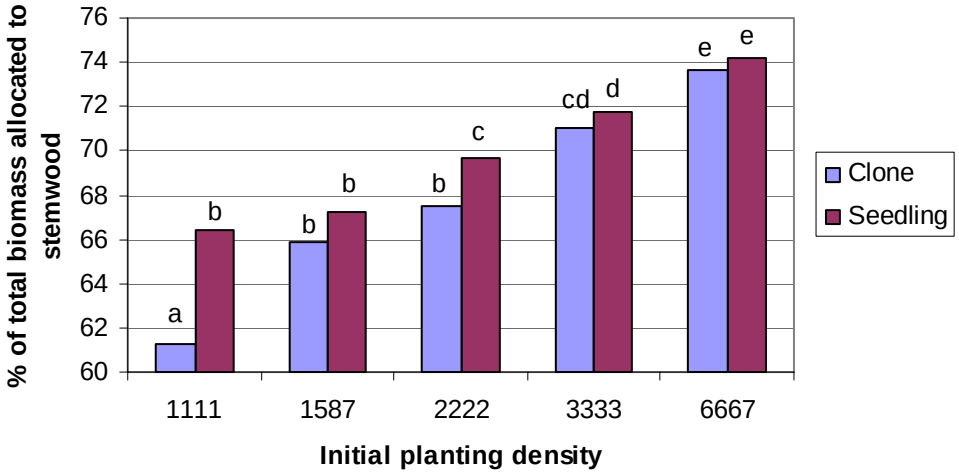


Figure 101: Percentage of total biomass allocated to stem wood in 1999

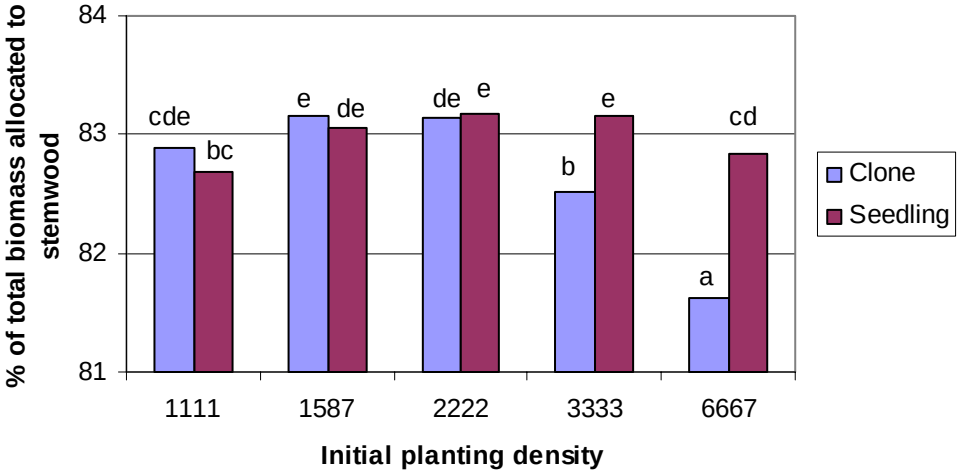


Figure 102: Percentage of total biomass allocated to stem wood in 2002

Chapter 5. Discussion

5.1. Competition

"Competition is an interaction between individuals, brought about by a shared requirement for a resource in limited supply, and leading to a reduction in the survivorship, growth and/or reproduction of the competing individuals concerned" (Begon *et al*. 1990).

The aim of this thesis was to describe and compare competition processes in even aged stands of the *Eucalyptus* genotypes tested. This has been done by comparing treatments within an experiment that tests the effect planting density and genotype had on timber production and stand dynamics through time. The simplest method of evaluating competition effects in forest stands is through the use of spacing trials. Spacing trials create stands/plots in which all silvicultural and climatic variables are constant. Changes in vigour and distribution of this vigour within and between treatments can then be attributed to competition alone. “Quantification of the symmetry and two-sidedness of competitive outcomes has been carried out experimentally by growing plants at different densities and in competition for one or more resources (Brand and Magnussen, 1988)”. This means that increased planting density was used to simulate increased competition between individuals. Therefore it was critical to prove that increased planting density resulted in a change in the degree of competition experienced between individuals within the stand. More specifically it needed to be proved that by increasing planting density, the level of competition was increased. Therefore the first hypothesis, which states, “Increased stand density results in increased competition between individuals within the stand”, needed to be accepted before any further analysis or comparisons could be carried out.

To accept this hypothesis it needed to be proven that increased planting density resulted in a reduction in the vigour of plots at an age where the mean tree size per plot was equal. It was shown that an increase in planting density at an equal mean tree size ($0.007m^2$) resulted in a decrease in vigour. The same trend was observed at a mean basal area of $0.009m^2$ and $0.015m^2$. Hypothesis 1 was therefore accepted.

Competition effects can be observed and analysed at a number of levels, from the responses of individual trees to the effects of competition on the dynamics of the stand (Tomé et al. 1994).

5.1.1. Individual tree response to competition

Whilst deriving allometric relationships it could be seen that there was a strong relationship between tree size (DBH) and SLA at age 5.5 years. In this relationship SLA increased with a decrease in DBH. At plot level, mean SLA was found to increase with an increase in planting density. This trend is consistent with that expected when resource pre-emption is a dominant form of competition being experienced (Newton and Jolliffe, 1998b). The clonal

treatments had a higher mean SLA than the seedling treatments at all planting densities. This simply means that the clone has a genetically driven propensity for higher SLA.

The difference in SLA between genotypes increased with an increase in planting density. This interaction was found to be highly statistically significant. The greater increase in mean SLA in clonal treatments than in the seedling treatments as a result of increased planting density is due to a greater number of smaller trees (with higher SLA) in the clonal plots at higher planting density. This is evident from the more positively skewed population in the high planting density clonal treatments than in the corresponding seedling treatments at both equal age, and at equal mean tree size.

The proportion of total biomass allocated to branches, is believed to be a good indicator of competition through resource pre-emption (Newton and Jolliffe, 1998b). A reduction in branch retention and branch production is believed to be a response to, and therefore an indicator of shade-induced reduction in light intensity (resource pre-emption). When the trial was destructively sampled at age 2.5 years in 1999, planting density was found to be highly significant in explaining the proportion of total biomass allocated to live branches at a stand level. In both genotypes, the proportional allocation of total biomass to branches decreased with an increase in planting density. This is in accordance with findings by Newton and Jolliffe (1998b). The clonal treatments allocated a significantly higher proportion of biomass to branches at both destructive sampling events. At the second destructive sampling event in 2002, the seedling treatments displayed the same trend of decreasing allocation to branches with increasing planting density. There was however no discernable interaction between planting density and allocation of biomass to branches in the clonal treatments at this sampling event.

These adjustments to the phenotypic characteristics of trees at different planting densities, provides further evidence to accept hypothesis 1, which states, “Increased stand density results in increased competition between individuals within the stand”. These adjustments furthermore suggest that resource pre-emption is the dominant competition process (mainly for light). By definition, resource pre-emption is asymmetrical in nature. This lends support for the acceptance of hypothesis 2, which states, “Larger trees use disproportionately more resources than smaller ones and therefore competition is asymmetrical”

5.1.2. Size class response to competition

The three biggest trees per plot (dominant trees) were found to be statistically significantly more vigorous in terms of mean basal area growth than the rest of the trees within those plots at 0.007 m^2, 0.009 m^2 and 0.015 m^2 mean basal area respectively. The greater vigour of the larger trees indicates that resources limiting growth are not utilised in proportion to the size of the tree. Rather, larger more dominant trees utilise disproportionately more resources than their smaller neighbours. Therefore as per the definitions of competition symmetry put forward by Von Euler *et al*. (1992) and Brand and Magnussen

(1987), the competition being experienced is asymmetrical. The second hypothesis stating, “Larger trees use disproportionately more resources than smaller ones and therefore competition is asymmetrical”, is accepted.

The mean RPR and RGR of the three biggest trees per plot at mean dominant basal areas of 0.013 m^2 and 0.022 m^2 respectively were analysed in terms of planting density to determine whether or not the increased presence of smaller trees was slowing the growth of the larger competitors. If RGR is accepted as the measure of vigour, then it can be stated that the smaller trees did in fact reduce the growth rate of the larger trees to some extent. Therefore it could be stated that there is a degree of competition from below, and that competition is two-sided. Therefore the third hypothesis could be accepted. Conversely using RPR as the measure, it was found that smaller trees did not reduce the vigour of larger dominant trees, therefore the third hypothesis which states, “When trees in a stand are competing for resources, smaller competitors take up some of the resources required by the larger ones, thereby slowing their growth, therefore competition is two sided”, would have to be rejected. RGR has been used by many authors when analysing competition in trees (Cannell *et al*. 1984; Petersen *et al*. 1990; Ford and Diggle, 1981; Stoll *et al*. 1994). RPR is the more contemporary measure of vigour (Brand and Magnussen 1988; Newton 1990; Newton and Jolliffe 1998b) and has been used by authors who claim that RGR does not appear to be independent of size in perennial plants.

There was no statistically significant interaction between planting density and genotype, when analysing the mean vigour of the 3 biggest trees per plot. This means that there is no difference in the degree of competition from below in the clonal and seedling plots. Therefore the fourth hypothesis stating, “suppressed trees in the clonal treatments reduce the growth of larger competitors to a greater extent than do the suppressed trees in the seedling treatments” had to be rejected. For this hypothesis to have been accepted, there needed to be a trend for vigour to decrease with an increase in planting density (true for RGR, and false for RPR), and more importantly the rate of decrease in vigour with a corresponding increase in planting density would have had to be significantly higher in the clonal treatments than in the seedling treatments. This was however not the case.

5.1.3. Stand level response to competition

Response to competition at a stand level can be measured in a number of ways, namely; degree of variability (CV%) within plots as used by Brand and Magnussen (1988), Bouvet (1997), Little (1999), Tome et al. (1994) and Von Euler et al. (1992), size-class distribution (skewness) of individuals within different treatments as used by Brand and Magnussen (1988), mortality/survival and finally production (volume or basal area).

The degree of variability in tree size was measured using CV% at both equal age and equal mean tree size. At equal age the variability in both height and basal area were analysed. Height measurements were made from age 0.2 years onwards, whereas DBH was only measured from age 1 year (could not be measured before as there was no breast height on these trees). When

looking at CV% for height over time it can be seen that CV% was initially high, then decreased, and increased again with time. This is similar to the trend observed by Tomé *et al*. (1994), Bouvet (1997), Von Euler *et al*. (1992) and Little (1999). This increase was greater in the clone than in the seedling, with the two highest planting densities experiencing the greatest increase in CV%, and the other planting densities remaining equal to one another as time has progressed. A similar trend in CV% was observed in basal area over time, with CV% increasing with time, this increase being higher in the clonal than the seedling treatments, and the two highest planting densities having the highest CV%, with no significant difference between the other planting densities through time.

Variation was measured (CV%) at an equal mean tree size per plot of 0.007 m^2 and 0.009m^2 respectively. At 0.007 m^2 mean basal area, the CV% in clonal treatments was statistically greater than in seedling treatments. The CV% in clonal treatments at 0.009m^2 was also higher than the seedling treatments, however this difference was not statistically significant. At 0.007 m^2 mean basal area, the 6667 stems.ha^{-1} planting density in the seedling and clonal treatments, had a significantly higher degree of variation than the 3333 stems.ha^{-1} plots, which in turn had a significantly higher degree of variation than all the other treatments. The only statistically significant difference in variation between genotypes at the same mean basal area and same planting density occurred in the 6667 stems.ha^{-1} treatment, where the variation in the clonal treatment was significantly higher than in the seedling treatments.

At mean basal area of 0.007m^2 and 0.009m^2 respectively, the trend was for skewness to increase with an increase in planting density. This corresponds with findings by Brand and Magnussen (1988), who also used the strategy of comparing variation and skewness at equal mean tree sizes, in *Pinus resinosa* (red pine). Skewness was calculated per plot at each measurement event. Skewness increased with planting density in both genotypes. The rate and magnitude of increase was higher in the clone than in the seedling. Skewness was found to increase to a greater extent in the higher planting density treatments (6667 stems.ha^{-1} and 3333 stems.ha^{-1}).

Survival and mortality were closely monitored through time. Survival percentage was calculated for each measurement event and analysed. At age one year, neither initial planting density nor its interaction with genotype, could explain a statistically significant portion of the variation in survival percentage. The initial survival (up to age 1) on the seedling was better than the clone. As time progressed planting density explained more and more of the variation in survival percentage and the survival of the clonal material surpassed that of the seedling material. However, survival percentage is not the correct statistic to use when quantifying survival/mortality in spacing trials, as applying a percentage when the denominators are unequal (initial planting density), can confound the results.

The purpose of this thesis is not to analyse and understand planting technique and or plant quality. Mortality in the first year after planting was predominantly as a result of plant quality, planting technique or both and not competition.

This was particularly true in the clonal treatments as this was one of the first times, *Eucalyptus* clonal cuttings were planted in the Kwa-Zulu Natal Midlands. Cuttings are a lot less robust and therefore more sensitive to transplanting than seedlings. The people doing the planting were not familiar with the correct planting techniques for cuttings and hence the higher initial mortality in the clones. Mortality after age one year was considered more likely to be as a result of competition. This concurs with Brouard and John (2000), who while working with *Eucalyptus grandis* x *Eucalyptus urophylla* hybrid clones in Brazil found that "Spacing treatment effects were non-significant at age one year, suggesting that competition effects intensified after age one year".

Therefore mortality after age one was analysed, and it was found that mortality occurred mainly in the seedling treatments. Planting density and its interaction with genotype was highly significant in explaining the mortality experienced after age one, with the highest mortality occurring in the highest planting density seedling treatments.

The relationship between mean tree size and surviving stems per hectare was considered as described by Yoda *et al*. (1963 as cited by Zeide 1985). It was found that an increase in mean tree size is accompanied by a reduction in survivorship. In the clonal treatments there is very little reduction in survivorship, however there is also very little increase in mean tree size. The actual slope of the line was not calculated as this a subjective process.

Zeide (1985) and Bi et al (2000) converted the relationship between mean tree size and surviving stems per hectare to explain the relationship between production per hectare and survival. It was found that this conversion of Yoda's –3/2 power rule, to explain production per hectare rather than mean tree size, is not applicable to the clone tested, as it is clear that the clonal plots have managed to increase production per unit area through time, without a reduction in survivorship.

At a stand level, all three measures tested, namely; CV%, skewness and mortality, need to be considered in conjunction with one another to better understand the processes at work.

- For example in the clonal treatments: As ramets have competed with one another, some have become dominant, and others suppressed. With time the number of suppressed trees has increased, thereby resulting in the population becoming more positively skewed. This positive skewness has been further enhanced by the low mortality of these suppressed trees. The positive skewness has the effect of reducing the mean tree size. The high survival together with increased skewness has resulted in the degree of variation in the high planting density treatments exceeding that in the low planting density treatments.
- Conversely, in the seedling treatments as time has progressed size class differentiation has occurred, however unlike in the clonal treatments, the suppressed individuals were more likely to die. This tendency for suppressed individuals to die has resulted in a lesser degree of positive skewness, and variation within the population at high planting densities

than that seen in the clonal treatments. The lesser degree of positive skewness also means that the mean tree size is larger.

The self-thinning law in its traditional sense does not apply to clones. Rather than mortality occurring as a result of competition, and mean tree size increasing thereafter, there is increased size class differentiation, with more and more trees being overtopped and suppressed (little or no subsequent growth from these individuals). This positive skewness in the population reduces the average tree size. However by staying alive these trees still contribute to the stem-wood on the stand, and therefore as the dominants and intermediates continue to grow there is a net increase in volume production per unit area, without a reduction in survivorship.

5.2. Production

Both full-tree and utilisable volume, mean annual increment and current annual increment were calculated at each measurement event. The seedling treatments and clonal treatments behaved very differently with regard to changes in planting density. In the seedling treatments, there was no statistically significant difference in volume production (full tree or utilisable) between the four highest planting density treatments. The 1111 stems.ha^{-1} treatments consistently produced statistically significantly less volume than the other planting density treatments. In the clonal treatments on the other hand there was a far wider spread in terms of volume production per planting density treatment. The most important aspect of these findings is the fact that in the case of this *Eucalyptus grandis* seedling crop, as long as you plant sufficient stems per hectare to start with (above a certain threshold – 1111 stems.ha^{-1} in this case) you can expect the same production irrespective of planting density. However as found by Brouard and John (2000) the clone appears to be extremely sensitive to planting density in terms of volume production.

Chapter 6. Recommendation and conclusion

From these results it is clear that clones and seedling react in very different ways to competition. The large differences in population dynamics observed, mean that we cannot just apply knowledge built up over the years regarding the management of *Eucalyptus grandis* and other plantation species to *Eucalyptus* hybrid clones. These differences will have direct implications on the way in which we measure, model and manage our clonal plantations in the future. The selection of clones will need to be done in conjunction with silvicultural research. The current practice is for clonal material to be selected according to its performance under current silvicultural regimes (based on what we do with *Eucalyptus grandis*). We may however be missing a trick here, in that we may be able to attain even better production from clonal material if we used a series of management regime by clonal trails to select the best clones together with the best silvicultural regime for that clone.

Chapter 7. References

7.1. Literature used

Archibald, D.J., & Bowling, C. 1995. Jack Pine Density Management Diagram for Boreal Ontario. OMNR, Northeast and Northwest Science and Technology. Technical Note. TN-005. (NWST TN – 31). 20p.

Begon, M., Harper, J.L., & Townsend, C.R. 1990. Ecology: Individuals, Populations, and Communities. 2nd Edition. Blackwell Scientific Publications, Oxford.

Bi, H., Wan, G., & Turvey, N.D. 2000. Estimating the Self-Thinning Boundary Line as a Density-Dependent Stochastic Biomass Frontier. Ecology. June, 2000. *www.findarticles.com/cf_0/m2120/6_81/63787055/print.jhtml*, 18 July 2001

Biging, G.S., & Dobbertin, M. 1995. Evaluation of Competition Indices in Individual Tree Growth Models. *Forest Science*. 41: (2) 360-377.

Bouvet, J. 1997. Effect of spacing on juvenile growth and variability of *Eucalyptus* clones. *Canadian Journal of Forest Research* 27: 174-179.

Brand, D.G. & Magnussen, S. 1988. Asymmetric, two-sided competition in even-aged monocultures of red pine. *Canadian Journal of Forest Research* 18: 901-910.

Breedenkamp, B.V. 1988. An Analysis of Correlated Curve Trend Experiments in *Eucalyptus grandis. Dissertation submitted to the Faculty of the Virginia Polytechnic Institute and State University in partial fulfilment of the requirements for the degree of Doctor of Philosophy in Forestry.*

Breedenkamp, B.V. 1993.Top Height: A difinition for use in South Africa. South African Forestry Journal. 167: 55.

Breedenkamp, B.V. 2000. Plantation Inventory. Forestry Handbook. South African Institute of Forestry. 161-165

Brouard, J.S., & John, S.E.T.,Tree Spacing Affects Clonal Ranking in *Eucalyptus grandis* x *E. urophylla* Hybrids. Frontiers of Forest Biology: Proceedings of the 1998 Joint Meeting of the North American Forest Biology Workshop and Western Forest Genetics Association (ed: Alan K Mitchell *et al*.) Food Products Press, an imprint of the Haworth Press Inc., 2000. pp. 13-23.

Bruce, D. 1975. Evaluating accuracy of tree measurements made with optical instruments. For. Sci. 21: 421-426.

Cannell, M.G.R., Rothery, P., & Ford, E.D. 1984. Competition within stands of *Picea sitchensis* and *Pinus contorta*. *Ann. Bot*. 53: 349-362.

Coetzee, J.A., 1992. A revised tree volume table for short rotation *Eucalyptus grandis* timber crops*. ICFR Bull.* 9/92, Pietermaritzburg 5 pp.

Drew, T.J., & Flewelling, J.W., 1977. Some recent Japanese theories of yield-density relationship and their application to Monterey pine plantations. For. Sci., 23:517-534.

Drew, T.J., & Flewelling, J.W., 1979. Stand density management: an alternative approach and its application to Douglas-fir plantations. For. Sci., 25: 518-532.

Encyclopedia.com., *www.encyclopedia.com*

Fasoula, D.A. & Fasoula, V.A. 1997. Competitive ability and breeding. *Plant Breeding Reviews*. 14: 89-138.

FOA. 1998. Abstract of South African Forestry. Facts for the year 1996/97. *Forest Owners Association*. P.O.Box 1553. Rivonia 2128. South Africa.

Ford, E.D. 1975. Competition and stand structure in some even-aged plant monocultures. *J.Ecol*. 63: 311-333.

Ford, E.D., & Diggle, P.J. 1981. Competition for light in a plant monoculture modelled as a spatial stochastic process. Ann. Bot. 48: 481-500.

Gomez, K.A. & Gomez, A.A. 1984. Statistical Procedures for Agricultural Research. Second Edition. John Wiley and Sons, New York. 298-308.

Hara, T. 1992. Effects of the mode of competition on stationary size distribution in plant populations. Ann. Bot. 69: 509-513.

Knox, R.G., Peet, R.K., and Christensen, N.L. 1989. Population dynamics in loblolly pine stands: changes in skewness and size inequality. Ecology, 70: 1153-1166.

Little, K.M. 1999. The Influence of Vegetation Control on the Growth and Pulping Properties of a *Eucalyptus grandis x Eucalyptus camuldulensis* Hybrid Clone. *Thesis submitted for the degree of Doctor of Philosophy*. University of Natal, Pietermaritzburg, South Africa.

Magnussen, D.G. 1989. Effects of adjustments of competition bias in progeny trials with single-tree plots. For. Sci. 35: 532-547.

Merriam-Webster Collegiate Dictionary., www.merriam-webster.com

Mohler, C.L., Marks, P.L., & Sprugel, D.G. 1978. Stand structure and allometry of trees during self-thinning of pure stands. *J.Ecol*. 66: 599-614.

Newton, P.F. 1990. Initial size hierarchy development within second-growth black spruce stands. *Can. J. For. Res*. 20: 1720-1731.

Newton, P.F., & Jolliffe, P.A. 1993. Aboveground dry matter partitioning, size variation, and competitive processes within second-growth black spruce stands. Can. J. For. Res. 23: 1917-1929.

Newton, P.F. & Jolliffe, P.A. 1998a. Assessing processes of intraspecific competition within spatially heterogeneous black spruce stands. *Canadian Journal of Forest Research* 28: 259-275.

Newton, P.F. & Jolliffe, P.A. 1998b. Aboveground modular component responses to intraspecific competition within density-stressed black spruce stands. *Canadian Journal of Forest Research* 28: 1587-1610.

Pallett, R.N. and Mitchell, A.G., 1993. Forest land types of the Natal region. Sappi Forests Research (unpubl.)

Petersen, T.D., Ning, Z., and Newton, M. 1990. Dynamics of size structure in seedling stands of *Fraxinus mandshurica* in North-east China. Ann. Bot. 66: 255-263.

Sale, G. 2001. Report on the Biomass Characteristics Over Time in a 3.5 year old High Planting Density Trial, with *Eucalyptus grandis* and *a Eucalyptus grandis x Eucalyptus urophylla* Hybrid Clone. Research Document 3/2001. Sappi Forests. (unpubl.).

Stoll, P., Weiner, J., & Schmid, B. 1994. Growth variation in a naturally established population of *Pinus sylvestris*. Ecology, 75: 660-670.

Tomé, M., Tomé, J.A., Clara Araújo, M. & Pereira, J.S. 1994. Intraspecific competition in irrigated and fertilised plantations. *Forest ecology and Management*. 69: 211-218.

Von Euler, F., Baradat, P., &Lemoine, B. 1992. Effects of plantation density and spacing on competitive interactions among half-sib families of maritime pine. *Canadian Journal of Forest Research* 22: 482-489.

Weiner, J. 1985. Size hierarchies in experimental populations of annual plants. Ecology, 66: 743-752.

West, P.W., & Borough, C.J. 1983. Tree suppression and the self-thinning rule in a monoculture of *Pinus radiata* D.Don*. Ann. Bot*. 52: 149-158.

White, J., & Harper, J.L. 1970. Correlated changes in plant size and number in plant populations. J. Ecol., 58: 467-485.

Williams, M.S., & Schreuder, H.T. 2000. Guidelines for Choosing Volume Equations in the Presence of Measurement Error in Height. *Canadian Journal of Forest Research* 30: 306-310.

Zeide, B. 1985. Tolerance and Self-tolerance of Trees. *Forest ecology and Management*. 13: 149-166.

7.2. Literature as cited by other authors, but not sourced

Binkley, D. 1984. Importance of size-density relationships in mixed stands of Douglas-fir and red alder. For. Ecol. Manage., 9: 81-85.

Clements, F.E., Weaver, J.E., & Hanson, H.C. 1929. Plant competition: analysis of community functions. Carnegie Inst., Washington, DC, Publ. 398.

Cochrane, L.A., & Ford, E.D. 1978. Growth of a Sitka spruce plantation: analysis and stochastic description of the development of the branching structure. J. Appl. Ecol. 15: 227-244.

Donald, C.M. 1968. The breeding of ideotypes. *Euphytica* 17: 385-403.

Duff, G.H., & Nolan, N.J. 1961a. Growth and morphogenesis in the Canadian forest species. IV. Radial growth in branches and main axis of *Pinus resinosa* Ait. under conditions of open growth, suppression and release. Can. J. Bot. 39: 385-410.

Duff, G.H., & Nolan, N.J. 1961b. Growth and morphogenesis in the Canadian forest species. V. Further studies of wood growth in branches and main axis of Pinus resinosa Ait. under conditions of open growth, suppression and release. Can. J. Bot. 39: 411-436.

Farrar, J.F. 1961. Longitudinal variation in thickness of the annual ring. For. Chron. 37: 323-330.

Harper, J.L. 1977. Population biology of plants. Academic Press, London, England.

Koyama, H., and Kira, T. 1956. Interspecific competition among higher plants. VIII. Frequency distributions of individual plant weight as affected by the interaction between plants. J. Inst. Polytech. (Osaka City University, Japan), Ser. D, 7: 73-94.

Lieffers, V.J. and Titus, S.J. 1989. The effect of stem density and nutrient status on size inequality and resource allocation in lodgepole pine and white spruce seedlings. Can. J. Bot. 67: 2900-2903.

Long, J.N. 1985. A practical approach to density management. For. Chron., 61: 23-27.

Makinen, H. 1996. Effect of intertree competition on branch characteristics of *Pinus sylvestris* families. Scand. J. For. Res. 11: 129-136.

McIntosh, R.P. 1980. The background and some current problems of theoretical ecology. Synthese, 43: 195-255.

Millington, W.F., & Chaney, W.R. 1973. Shedding of shoots and branches. *In* Shedding of plant parts. *Edited by* T.T. Kozlowski. Academic Press, New York. Pp. 149-204.

Pitelka, L.F. 1984. Application of the -3/2 power law to clonal herbs. Am. Nat., 123: 442-449.

Schwinning, S., & Fox, G.A. 1995. Population dynamic consequences of competitive symmetry in annual plants. Oikos, 72: 422-432.

Stiell, W.M. 1970. Some competitive relations in a red pine plantation. Dep. Fish. For., Can. For. Serv., Publ. 1272. 10 p.

Sultan, S.E. 1987. Evolutionary implications of phenotypic plasticity in plants. Evol. Biol. 21: 127-176.

Tadaki, Y., & Shidei, T. 1959. Studies on the competition of forest trees. II. The thinning experiment on small model stand of Sugi (*Cryptomeria japonica*) seedlings. J. Jpn. For. Soc., 41: 341-349.

Thomas, S.C., & Weiner, J. 1989. Including competitive asymmetry in measures of local interference in plant popuplations. Oecologia (Heidelb.), 80: 349-355.

Yoda, K., Kira, T., Ogawa, H., & Hozumi, K. 1963. Intra-specific competition among higher plants. XI. Self-thinning in overcrowded pure stands under cultivated and natural conditions. J. Bio. Osaka City Univ. 14: 107-129.

Watkinson, A. 1992. Plant senescence. Trees (Berl.), 7: 417-420.

Weiner, J. 1986. How competition for light and nutrients affects size variability in *Ipomoea tricolor* populations. Ecology, 67: 1425-1427.

Weiner, J., & Thomas, S.C. 1986. Size variability and competition in plant monocultures. Oikos, 47: 211-222.

Weiner, J. 1990. Asymmetric competition in plant populations. Trends Ecol. Evol. 5: 360-364.

Weiner, J., Wright, D.B., & Castro, S. 1997. Symmetry of below-ground competition between *Kochia scoparia* individuals. Oikos, 79: 85-91.

Wenger, K.F. (Editor), 1984. Forestry Handbook. John Wiley, New York, 2nd edn, 1335 pp.

Weller, D.E. 1987. A reevaluation of the –3/2 power rule of self-thinning. Ecol. Monogr. 57: 23-43.

West, P.W., Jackett, D.R., & Borough, C.J. 1989. Competitive processes in a monoculture of *Pinus radiata* D. Don. *Oecologia*, 81: 57-61.

White, J. 1980. Demographic factors in populations of plants. In: O.T. Solbrig (Editor), Demography and Evolution of Plant Populations. Blackwell, Oxford, pp. 21-48.

Williams, M.S., Bechtold, W.A., and La Bau, Y.J. 1994. Five instruments for measuring tree-height: an evaluation. South. J. Appl. For. 18: 76-82.

Appendix 1: Coefficients generated for predicting height using DBH

Age	Genotype	Planting Density	b_1	b_2	b_3
1.0	Clone	1111	6.54	0.401	1.31
1.4	Clone	1111	731	0.032	55
1.9	Clone	1111	11.8	0.198	3.19
2.5	Clone	1111	15.01	0.14	0.6
3.4	Clone	1111	20.6	0.21	5.72
4.4	Clone	1111	31.44	0.084	8.65
5.0	Clone	1111	28.71	0.118	7.9
5.5	Clone	1111	32.24	0.092	9.26
1.0	Clone	1587	6.85	0.37	1.5
1.4	Clone	1587	10.04	0.255	2.02
1.9	Clone	1587	12.3	0.195	3.2
2.5	Clone	1587	17.06	0.155	3.83
3.4	Clone	1587	24.41	0.131	5.98
4.4	Clone	1587	28.45	0.121	6.83
5.0	Clone	1587	31.13	0.112	7.51
5.5	Clone	1587	31.67	0.128	7.43
1.0	Clone	2222	6.5	0.466	1.25
1.4	Clone	2222	11.7	0.16	0.08
1.9	Clone	2222	13.84	0.252	4.53
2.5	Clone	2222	15.49	0.31	4.28
3.4	Clone	2222	47.3	0.064	12.7
4.4	Clone	2222	27.55	0.148	6.22
5.0	Clone	2222	29.79	0.12	6.68
5.5	Clone	2222	36.6	0.092	8.22
1.0	Clone	3333	6.29	0.587	1.33
1.4	Clone	3333	89	0.047	25
1.9	Clone	3333	18.8	0.16	5.42
2.5	Clone	3333	17.22	0.219	3.74
3.4	Clone	3333	21.66	0.244	5.25
4.4	Clone	3333	23.45	0.171	4.96
5.0	Clone	3333	27.47	0.181	6.32
5.5	Clone	3333	26.95	0.177	6.1
1.0	Clone	6667	6.364	0.833	1.33
1.4	Clone	6667	10.7	0.376	1.68
1.9	Clone	6667	11.26	0.446	2.47
2.5	Clone	6667	15.01	0.345	3.02
3.4	Clone	6667	21.9	0.24	4.53
4.4	Clone	6667	24.47	0.204	4.93
5.0	Clone	6667	26.92	0.186	5.4
5.5	Clone	6667	26.32	0.229	4.94

Age	Genotype	Planting Density	b_1	b_2	b_3
1.0	Seedling	1111	5.6	0.541	1.86
1.4	Seedling	1111	16.7	0.141	5.46
1.9	Seedling	1111	20.2	0.103	7.5
2.5	Seedling	1111	15.36	0.227	4.59
3.4	Seedling	1111	21.84	0.184	4.93
4.4	Seedling	1111	24.34	0.136	5.19
5.0	Seedling	1111	25.01	0.22	6.5
5.5	Seedling	1111	28.36	0.131	6.33
1.0	Seedling	1587	6.46	0.418	2.02
1.4	Seedling	1587	10.78	0.297	2.85
1.9	Seedling	1587	16.21	0.154	4.95
2.5	Seedling	1587	16.99	0.208	4.61
3.4	Seedling	1587	22.28	0.211	5.38
4.4	Seedling	1587	24.43	0.188	5.77
5.0	Seedling	1587	25.62	0.173	5.88
5.5	Seedling	1587	27.25	0.159	6.02
1.0	Seedling	2222	6.53	0.398	1.77
1.4	Seedling	2222	12.66	0.239	3.31
1.9	Seedling	2222	11.97	0.326	3.03
2.5	Seedling	2222	17.69	0.168	2.14
3.4	Seedling	2222	22.59	0.201	3.92
4.4	Seedling	2222	25.88	0.168	5
5.0	Seedling	2222	26.85	0.191	5.27
5.5	Seedling	2222	27.84	0.175	5.57
1.0	Seedling	3333	6.269	0.532	1.59
1.4	Seedling	3333	10.8	0.358	1.92
1.9	Seedling	3333	12.96	0.265	2.28
2.5	Seedling	3333	16.34	0.252	2.7
3.4	Seedling	3333	21.79	0.322	4.77
4.4	Seedling	3333	23.22	0.284	5.34
5.0	Seedling	3333	25.07	0.381	6.61
5.5	Seedling	3333	26.25	0.267	6.53
1.0	Seedling	6667	6.403	0.71	1.13
1.4	Seedling	6667	9.691	0.659	1.81
1.9	Seedling	6667	11.89	0.426	2.41
2.5	Seedling	6667	14.56	0.474	3.06
3.4	Seedling	6667	22.05	0.266	4.2
4.4	Seedling	6667	23.35	0.256	4.67
5.0	Seedling	6667	24.35	0.253	5.04
5.5	Seedling	6667	27.63	0.178	5.14

Appendix 2: Graphical representations of various allometric relationships described in Table 1

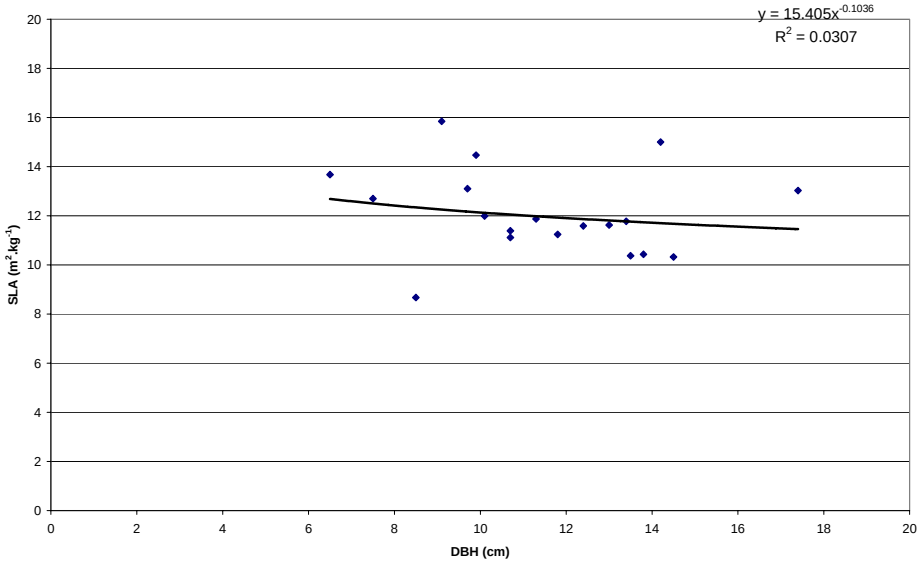


Figure 103: Relationship between DBH and SLA for the clonal treatments at age 2.5 years

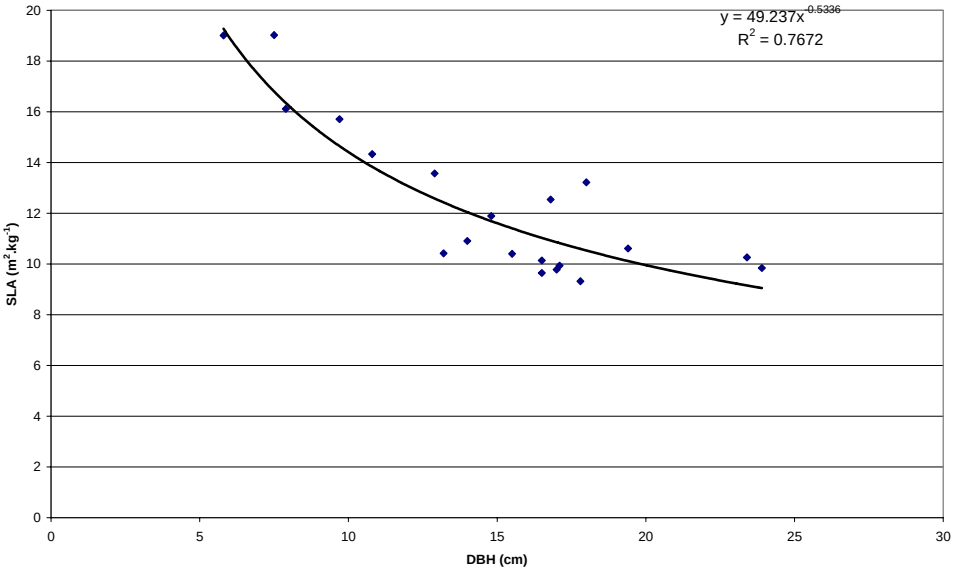


Figure 104: Relationship between DBH and SLA for the clonal treatments at age 5.5 years

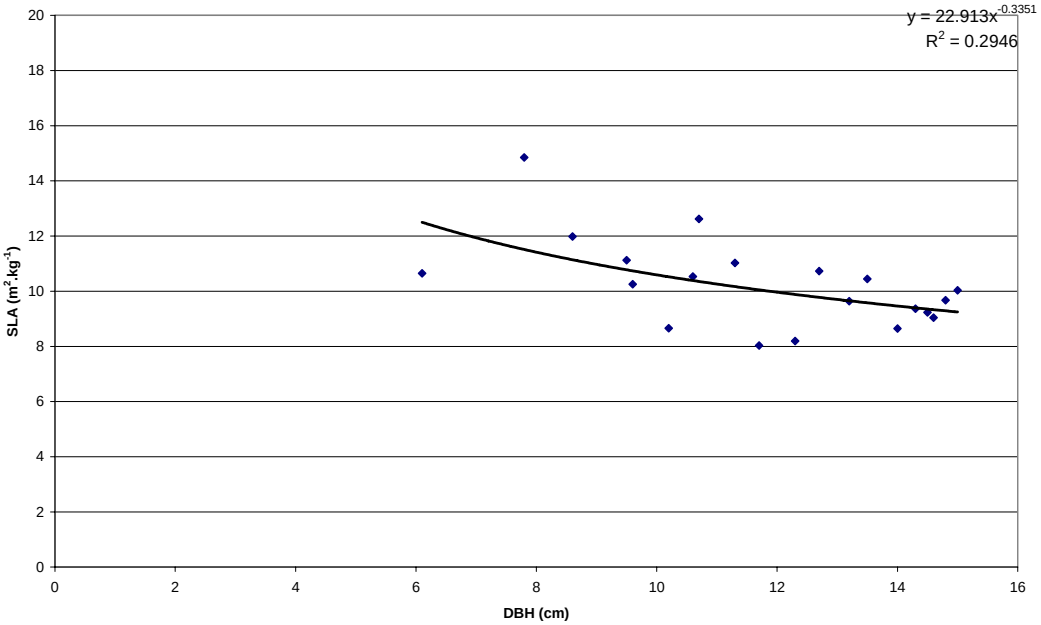


Figure 105: Relationship between DBH and SLA for seedling treatments at age 2.5 years

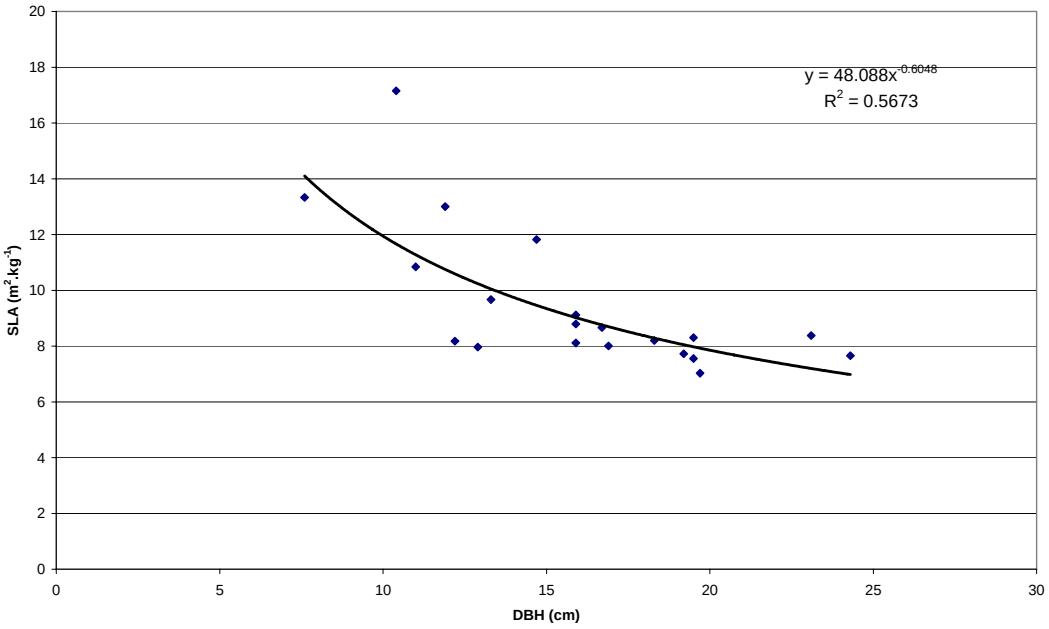


Figure 106: Relationship between DBH and SLA for the seedling treatments at age 5.5 years

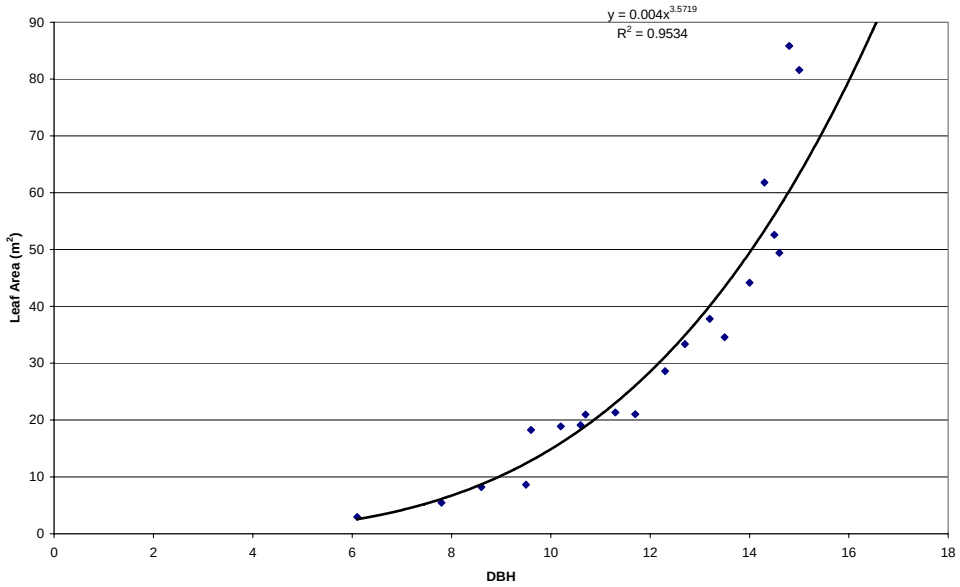


Figure 107: Relationship between DBH and leaf area for the clonal treatments at age 2.5 years

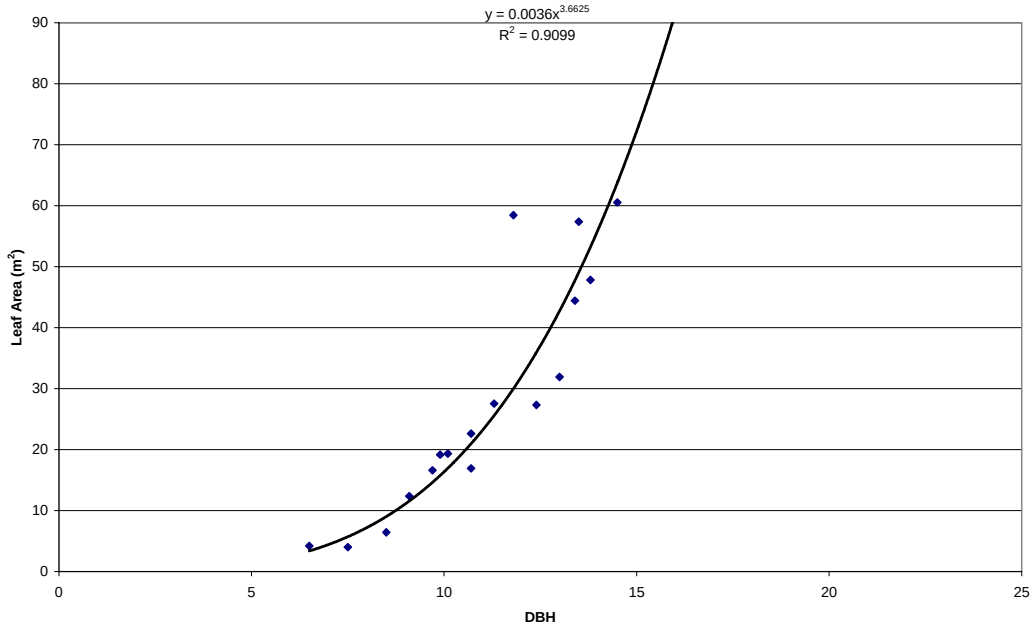


Figure 108: Relationship between DBH and leaf area for the seedling treatments at age 2.5 years

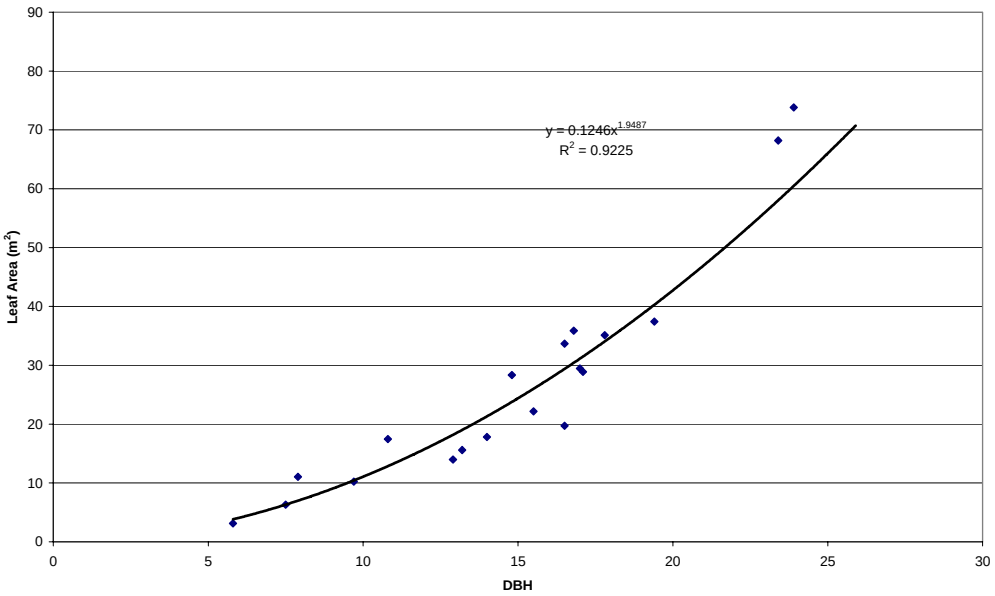


Figure 109: Relationship between DBH and leaf area for the clonal treatments at age 5.5 years

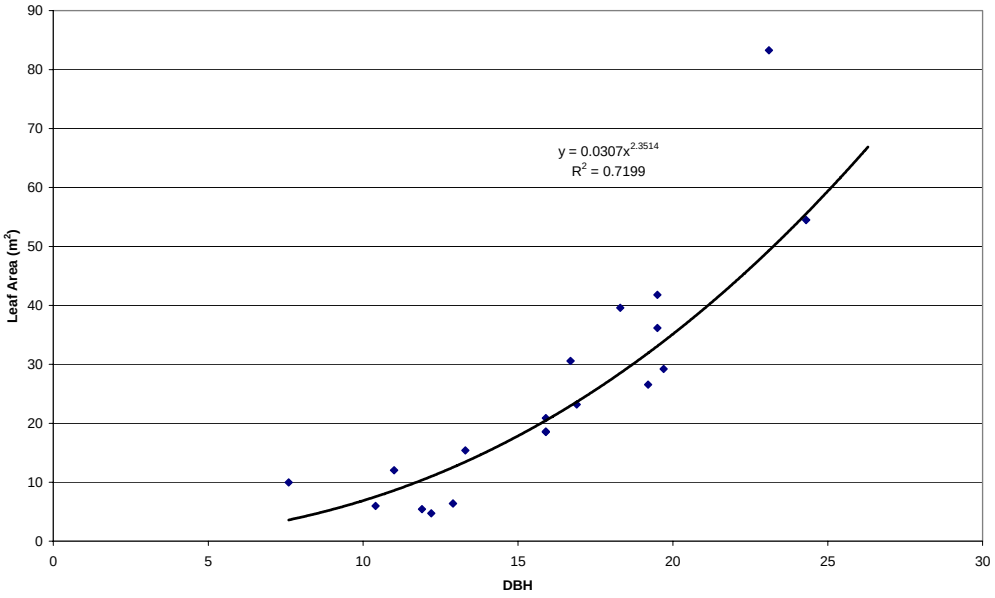


Figure 110: Relationship between DBH and leaf area for the seedling treatments at age 5.5 years

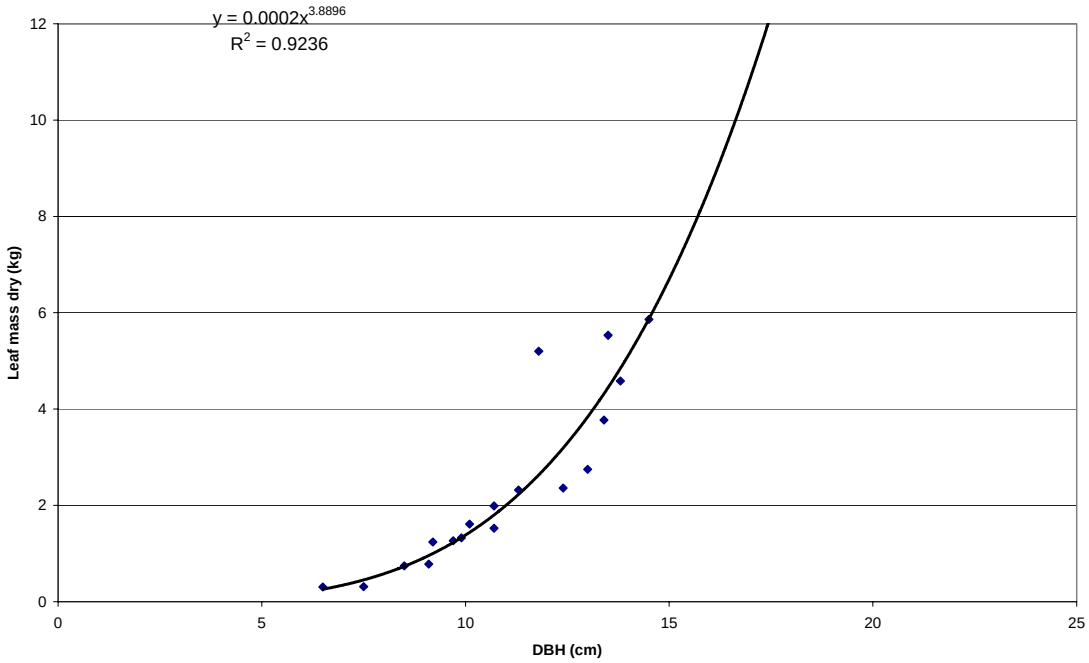


Figure 111: Relationship between DBH and leaf mass for the clonal treatments at age 2.5

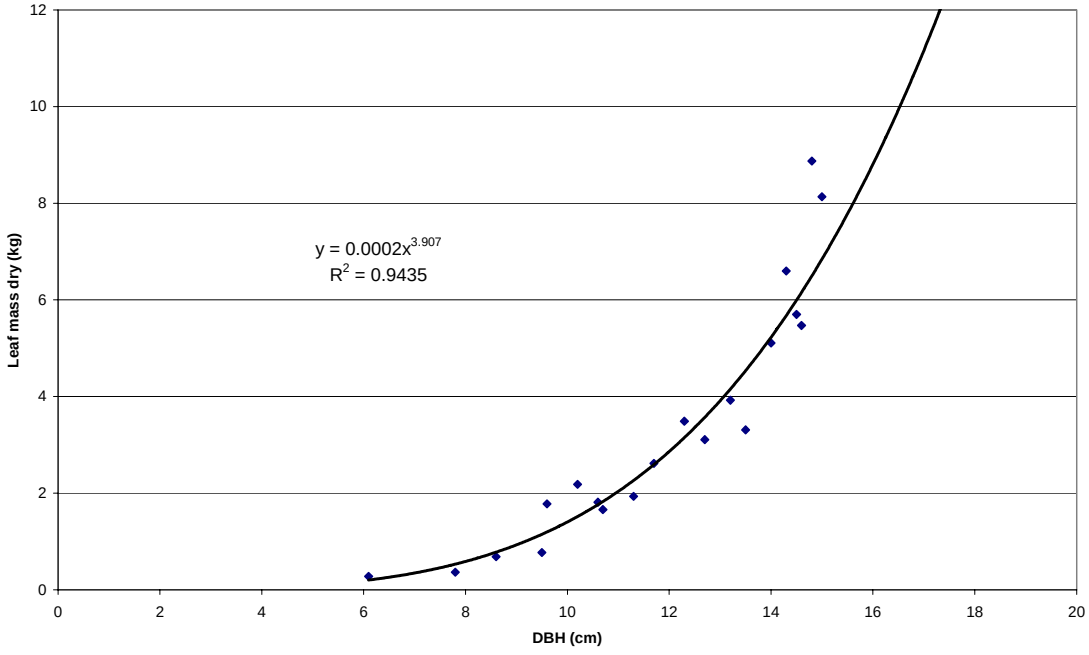


Figure 112: Relationship between DBH and leaf mass for the seedling treatments at age 2.5

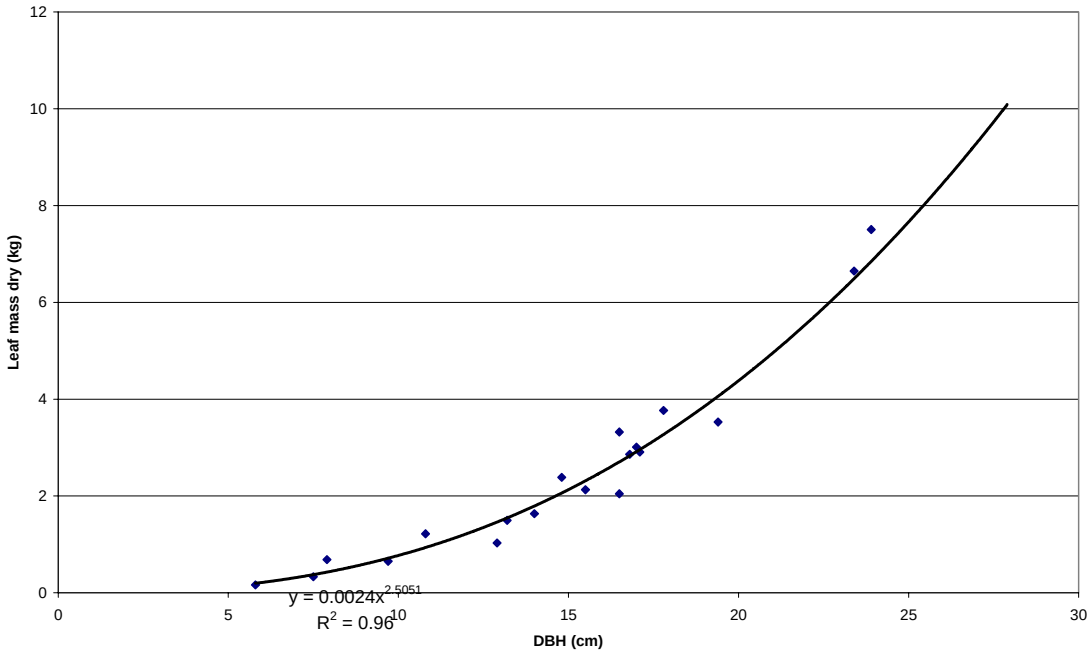


Figure 113: Relationship between DBH and leaf mass for the clonal treatments at age 5.5

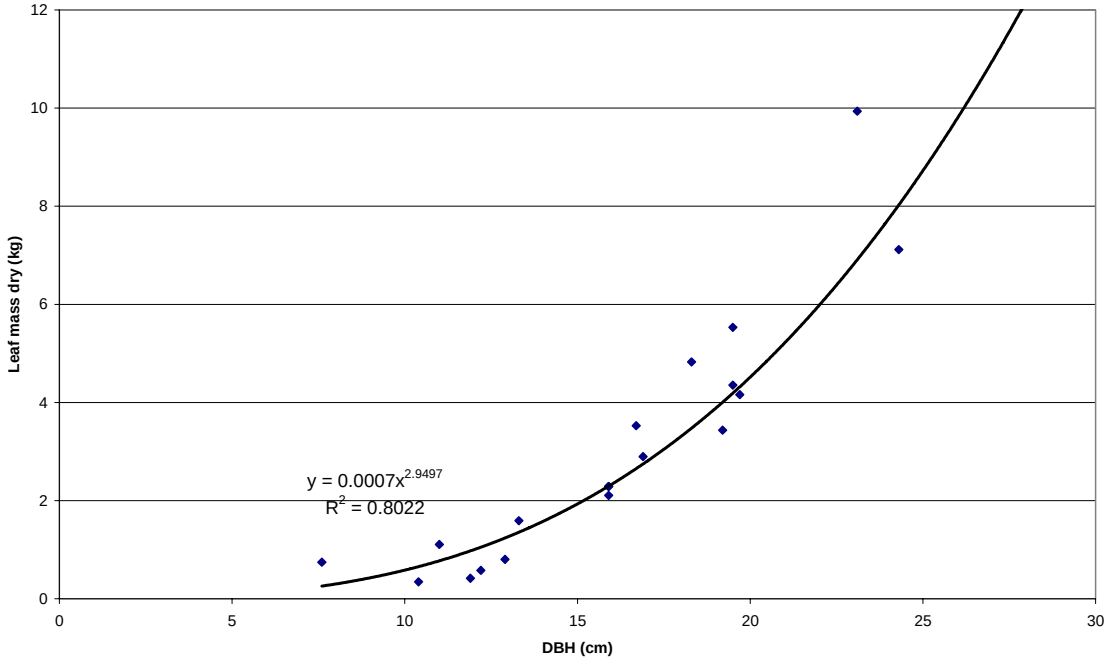


Figure 114: Relationship between DBH and leaf mass for the seedling treatments at age 5.5

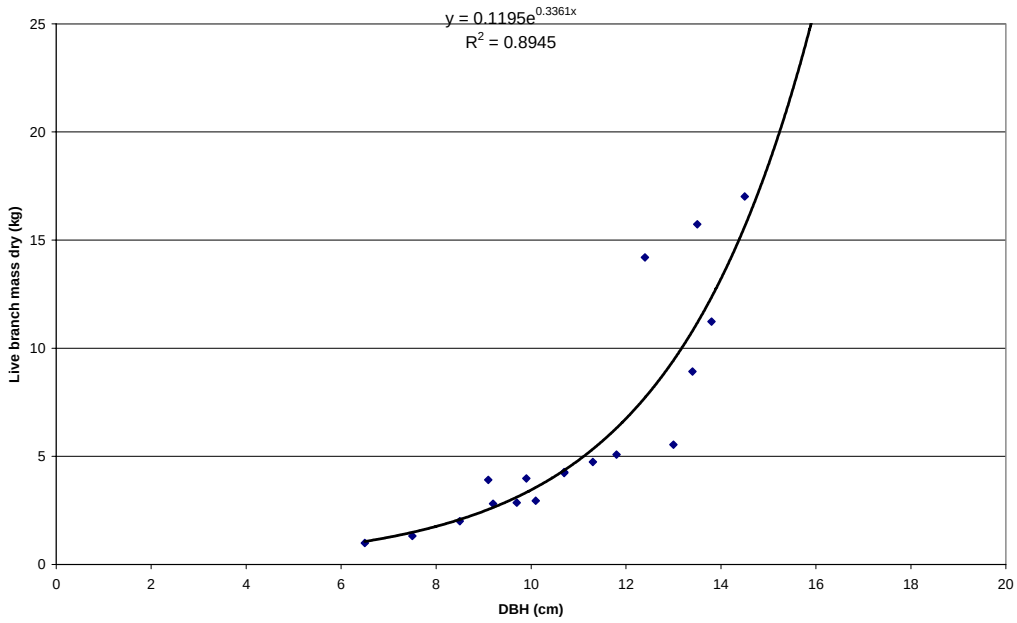


Figure 115: Relationship between DBH and live branch mass for the clonal treatments at age 2.5

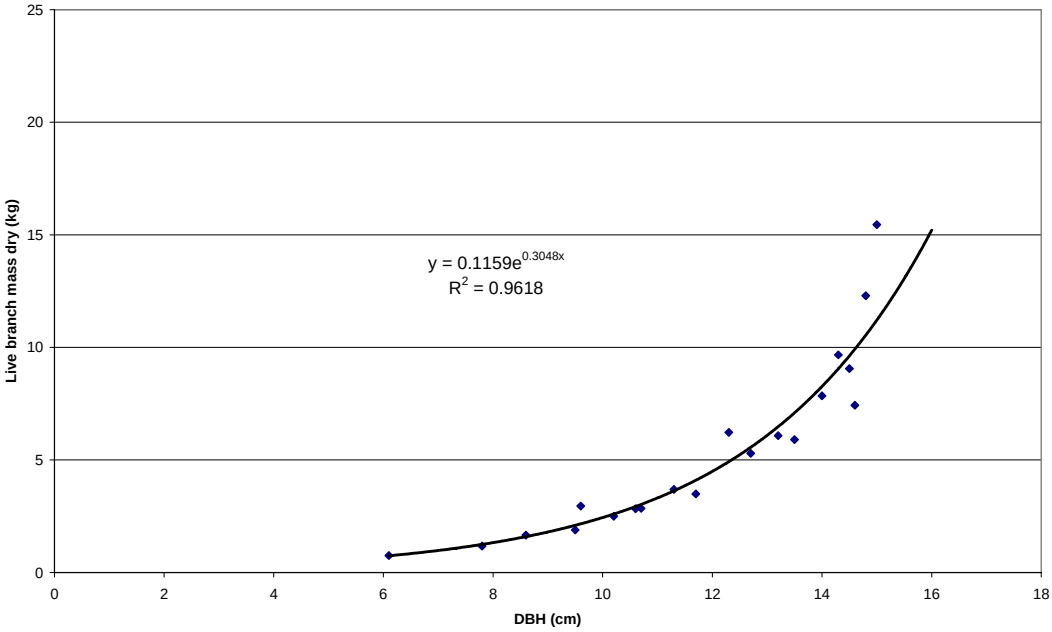


Figure 116: Relationship between DBH and live branch mass for the seedling treatments at age 2.5

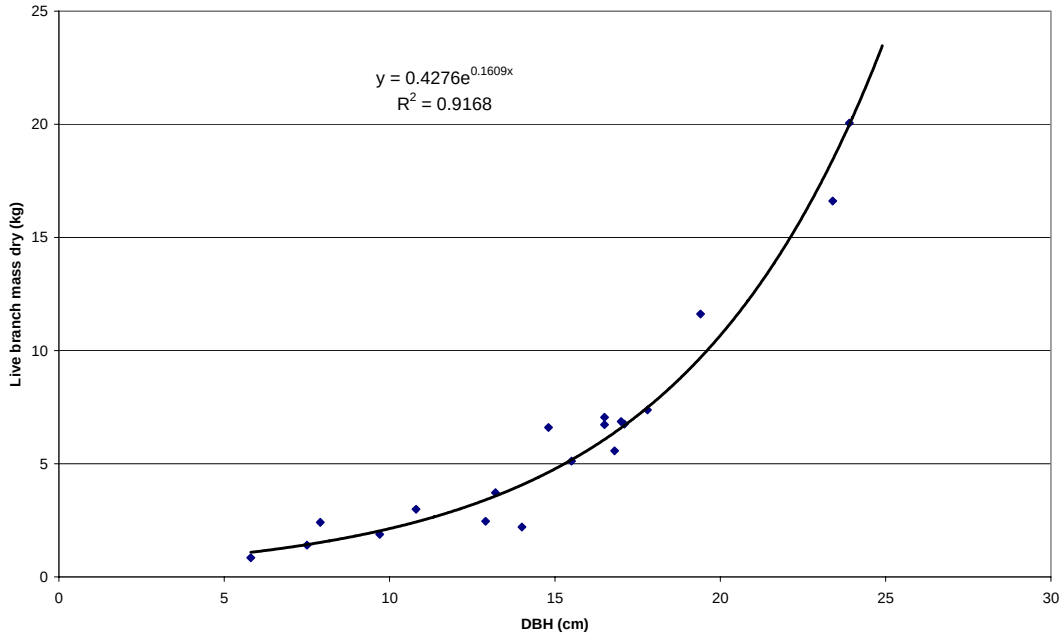


Figure 117: Relationship between DBH and live branch mass for the clonal treatments at age 5.5

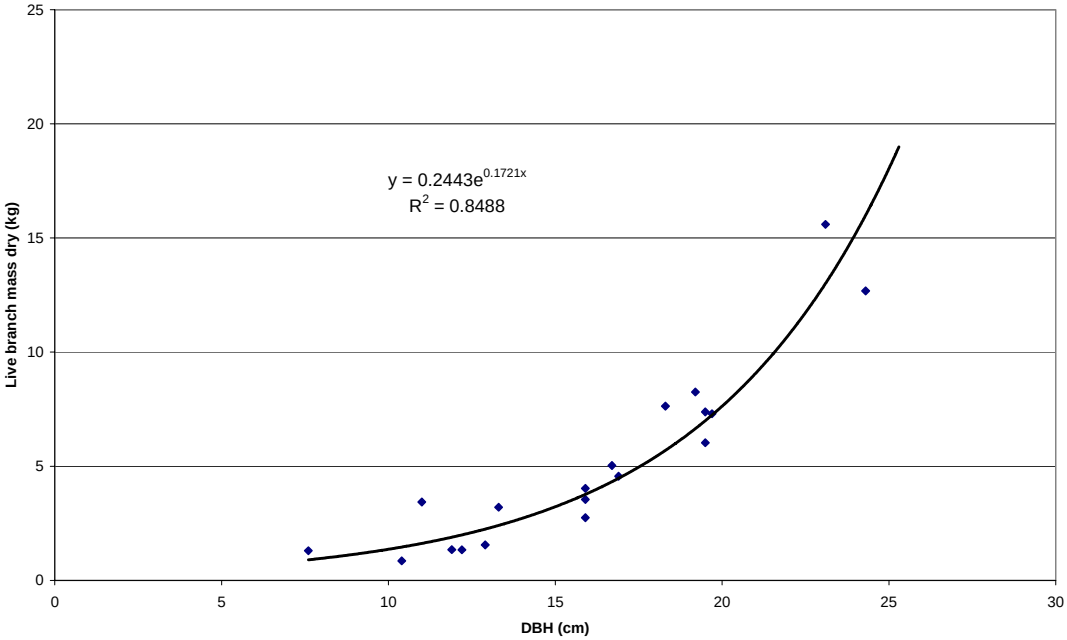


Figure 118: Relationship between DBH and live branch mass for the seedling treatments at age 5.5

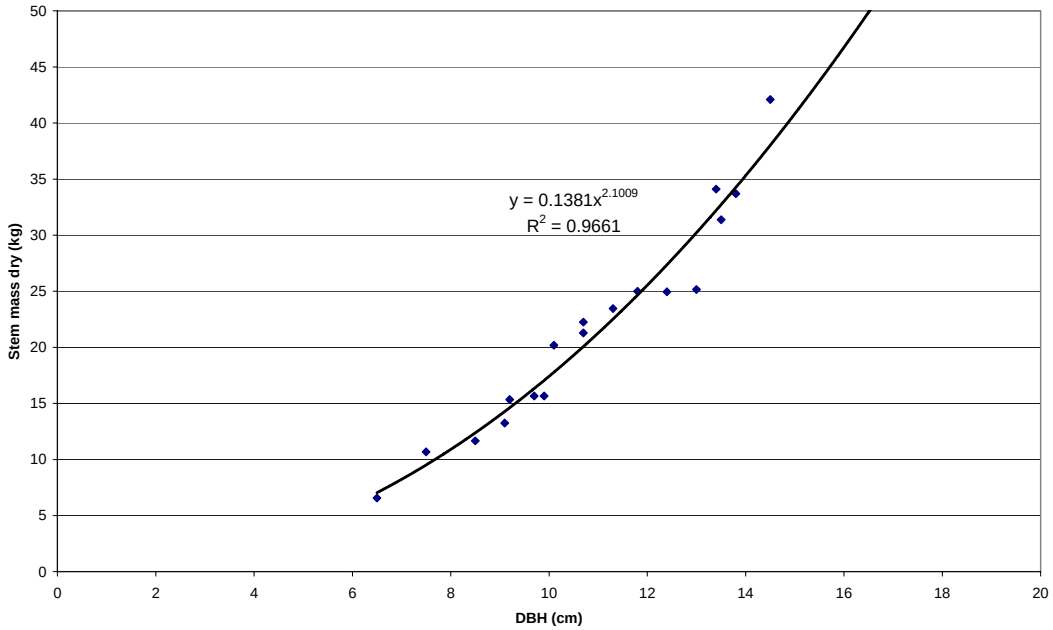


Figure 119: Relationship between DBH and stem dry mass for clonal treatments at age 2.5

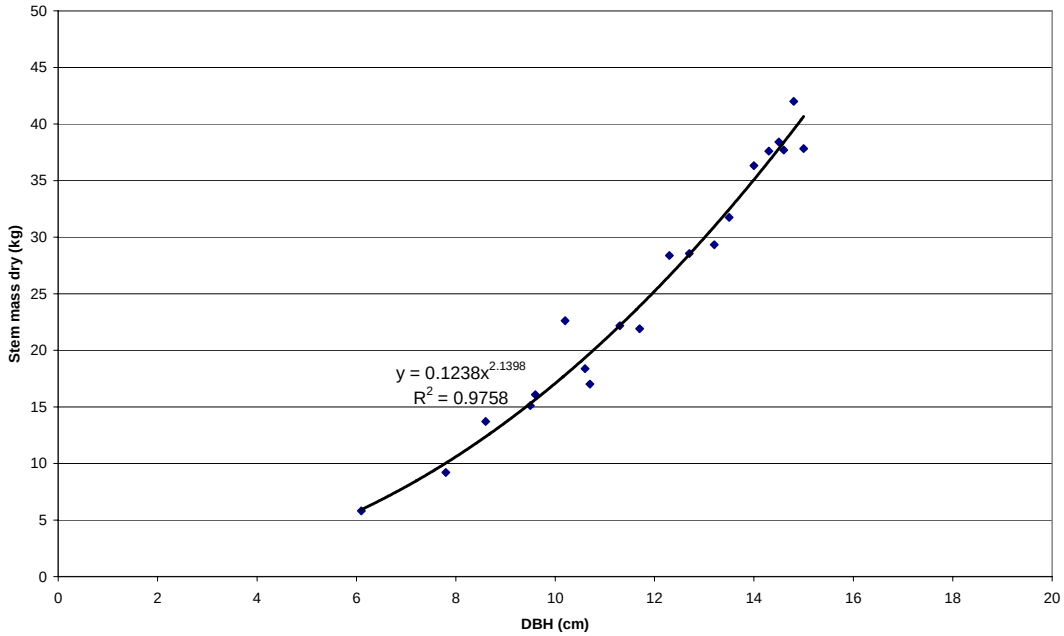


Figure 120: Relationship between DBH and stem dry mass for seedling treatments at age 2.5.

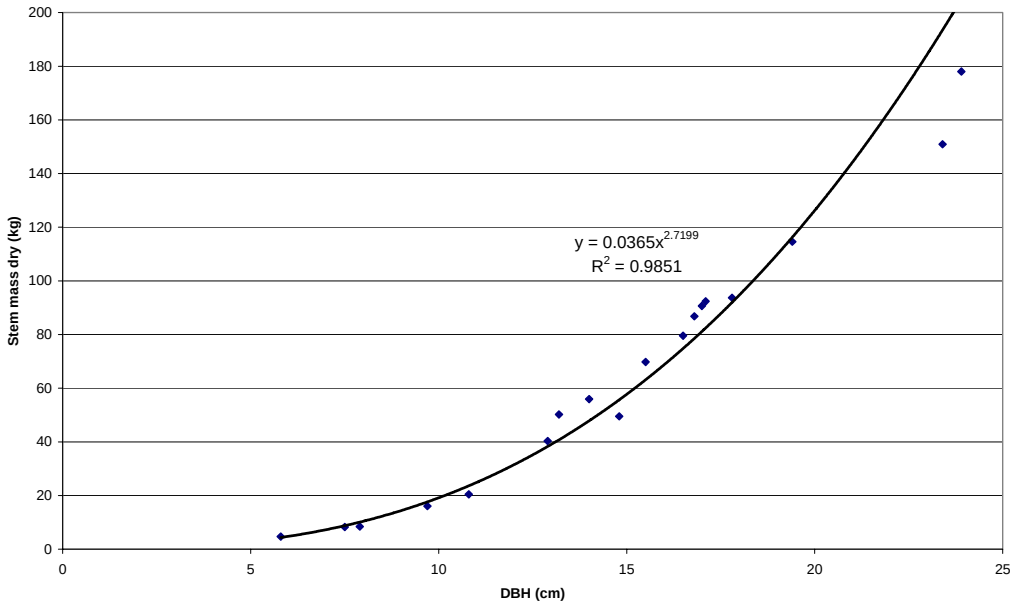


Figure 121: Relationship between DBH and stem dry mass for clonal treatments at age 5.5.

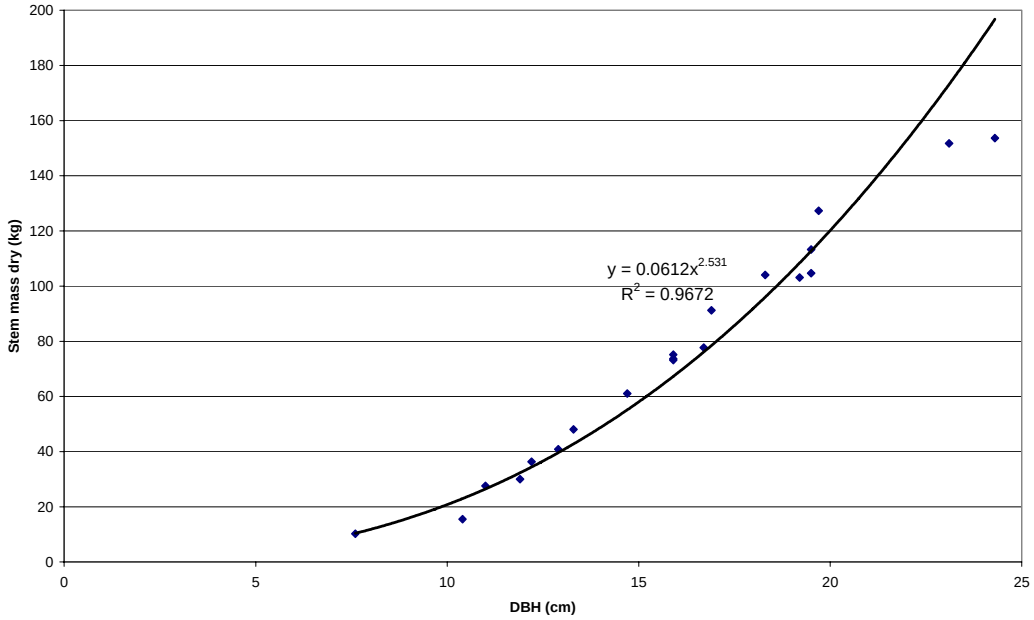


Figure 122: Relationship between DBH and stem dry mass for seedling treatments at age 5.5.

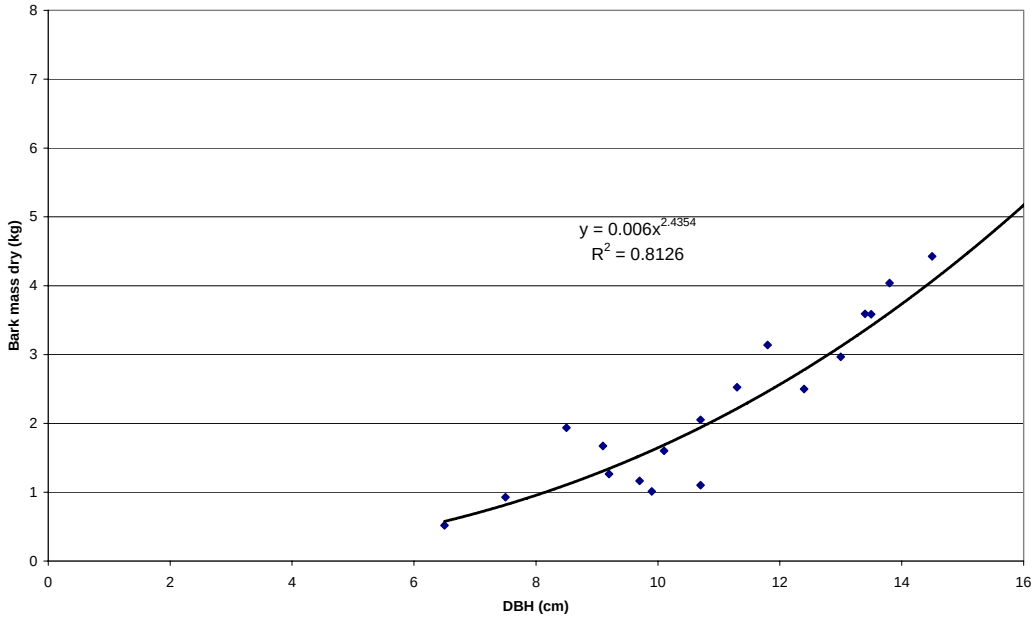


Figure 123: Relationship between dry bark mass and DBH for the clonal treatments at age 2.5 years

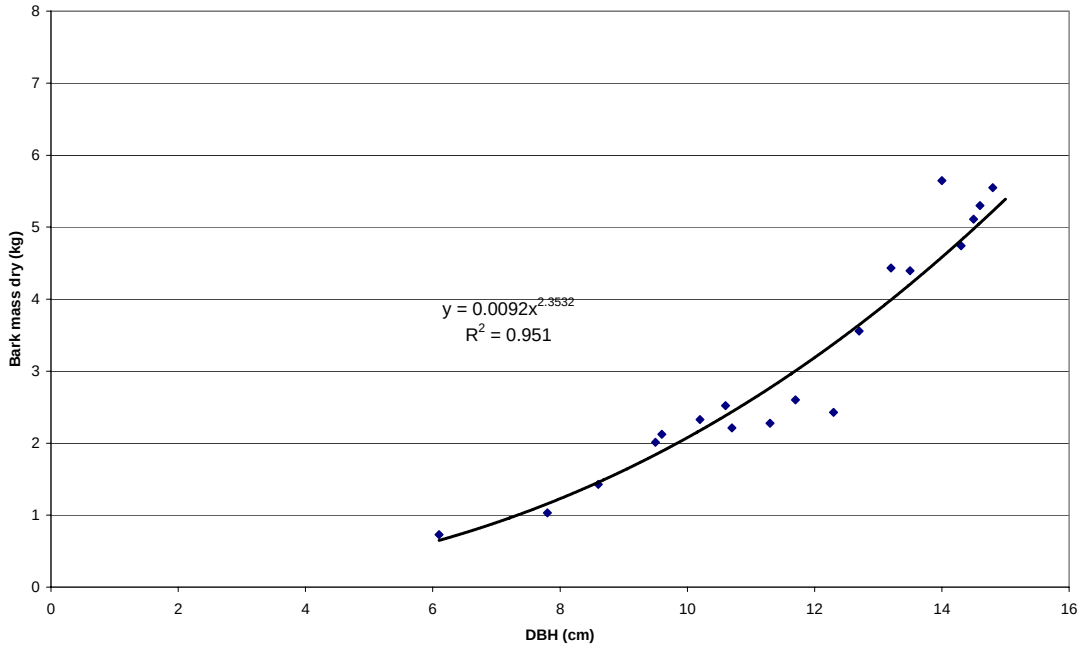


Figure 124: Relationship between dry bark mass and DBH for the seedling treatments at age 2.5 years

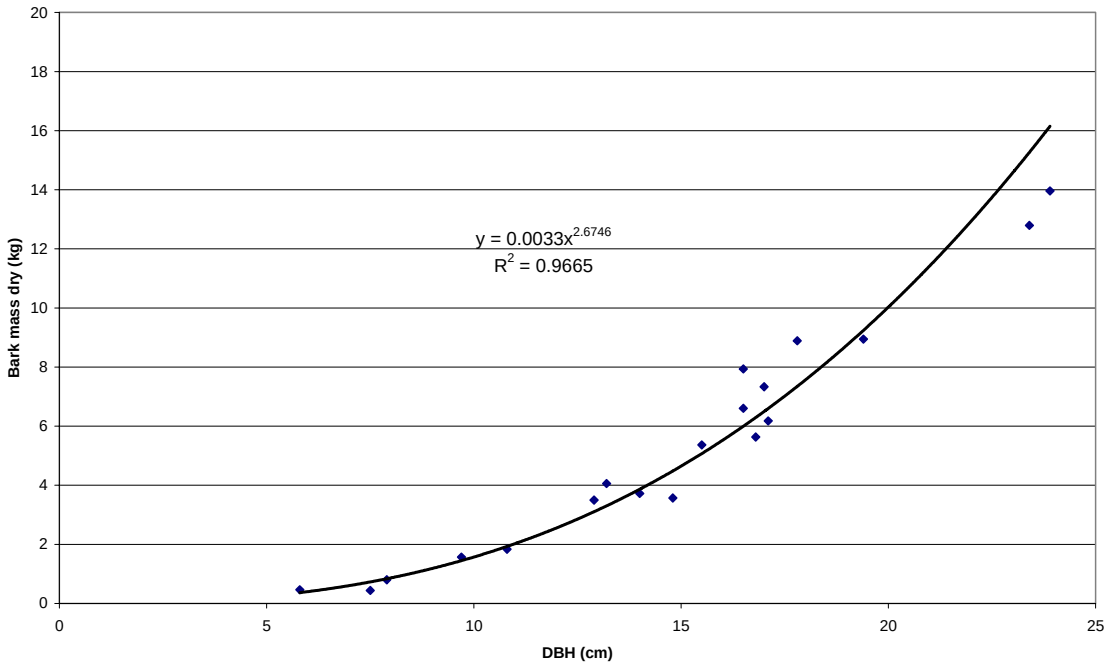


Figure 125: Relationship between dry bark mass and DBH for the clonal treatments at age 5.5 years

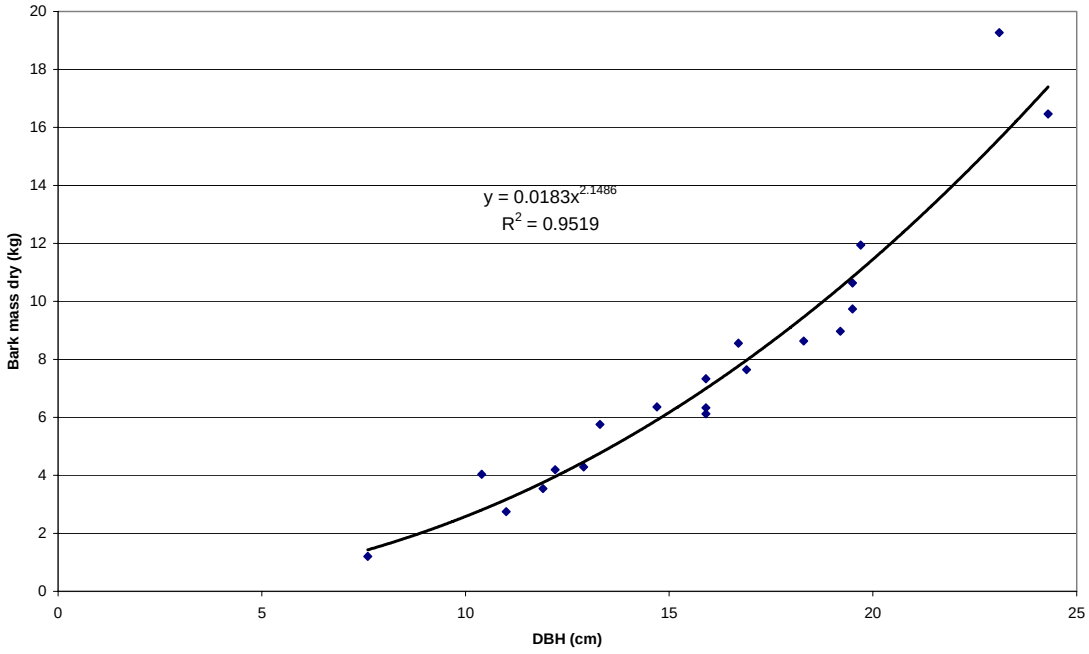


Figure 126: Relationship between dry bark mass and DBH for the seedling treatments at age 5.5 years

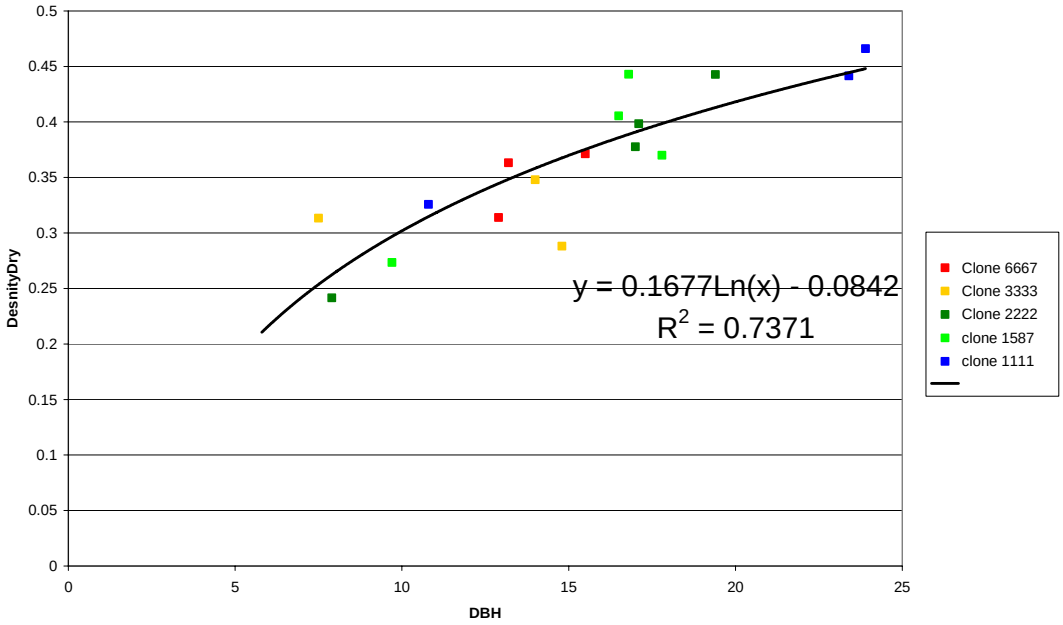


Figure 127: Relationship between DBH and stem wood density for the clonal treatments at age 5.5 years

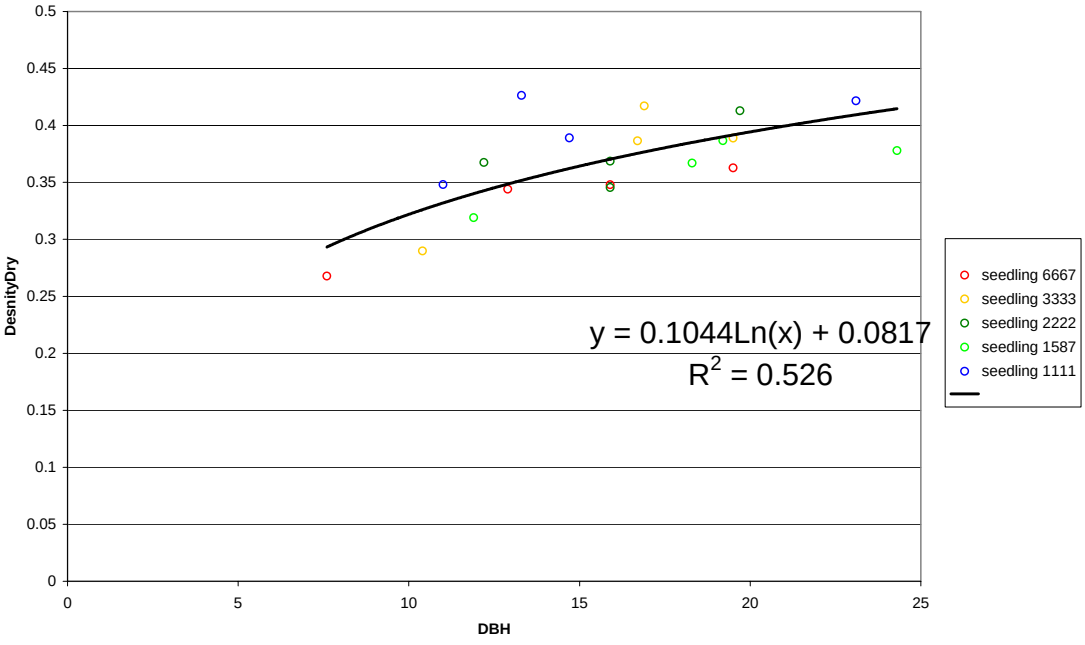


Figure 128: Relationship between DBH and stem wood density for the seedling treatments at age 5.5 years

Appendix 3: Individual DBH model

		Equation 1										Equation 2											
		Gompertz Coefficients				Linear Regression Coefficients						Gompertz Coefficients				Linear Regression Coefficients							
Tree-id	Description	B	M	C	A	b_0	b_1	b_2	b_3	b_4	Adjusted R^2	B_1	M_1	C_1	A_1	b_0_1	b_1_1	b_2_1	b_3_1	b_4_1	Adjusted R^2	Max Age	Node
1	Gomp no const	1.5057	0.7947	8.3496							99.9											5.50	
2	Gomp no const	0.4113	1.904	21.05							99.6											5.50	
3	Gomp no const	1.1585	0.9161	11.1895							99.9											5.50	
4	Spline	4.407	0.6415	3.50628							99.9	4.465	4.91	1.506	3.5							5.50	3.4
5	Gomp no const	13.08	0.8466	3.001																		1.92	
6	Straight line(no growth from age 1)					2.2																1.92	
7	Gomp with const	0.5388	-9.169	2426	-2411						99.8											5.50	
8	Gomp with const	0.006304	541.8	3.499E+12	2.161						52.3											5.50	
9	Gomp no const	1.7767	0.5952	7.5206							99.9											5.50	
10	Gomp with const	0.4007	-9.685	845.2	-828.6						99.9											5.50	
11	Gomp with const	2.678	-0.5852	117.9	-112.6						99.6											5.50	
12	Gomp with const	1.473	1.252	7.06	3.51						99.6											5.50	
13	Gomp with const	4.095	0.702	2.869	1.125						81.5											5.50	
14	Spline	2.563	0.195	5.196							97.4	4.029	4.96	0.4486	5.2							5.50	3.4
15	Gomp with const	3.138	-0.04082	22.43	-18.33						99											5.50	
16	Gomp with const	1.6875	1.4687	6.405	4.551						99.9											5.50	
17	Gomp with const	0.2601	-19.43	3925	-3900						99.6											5.50	
18	Dead before age 1																						
19	Gomp with const	1.961	-1.933	499.7	-493.7						97											5.50	
20	Gomp no const	1.539	0.67	7.5069							99.4											5.50	
21	Gomp with const	0.59	0.7299	4.36	0.59						92.1											5.50	
22	Gomp no const	0.7662	1.0043	12.882							99.8											5.50	
23	Gomp no const	1.6094	0.6957	7.8203							99.8											5.50	
24	Gomp no const	2.123	0.6405	5.5687							95.1											5.50	
25	Gomp with const	7.671	0.743	7.331	-3.096						95.2											3.41	
26	Gomp no const	2.79	0.5935	5.2923							99.5											5.50	
27	Gomp with const	1.53	1.201	4.543	3.599						99.7											5.50	
28	Gomp no const	1.4305	0.5949	8.1418							99.6											5.50	
29	Gomp with const	0.8101	1.356	10.89	2.12						99.9											5.50	
30	Gomp no const	1.778	-0.61	4.6687							73.6											5.50	
31	Gomp with const	1.072	1.654	8.58	3.857						99.7											5.50	
32	Gomp with const	1.9487	0.12	14.2	-7.9						99.7											5.50	
33	Spline	15.29	1.051	0.9924	4.009							3.847	4.639	1.141	5							5.50	3.4
34	Gomp with const	1.156	1.087	6.6	2.48						99.8											5.50	
35	Spline	3.568	0.6464	5.0859							99.5	0.076	-5.49	8.48							99.6	5.50	3.4
36	Gomp with const	1.58	-0.5	20	-14						95.3											5.50	
37	Gomp with const	1.179	1.471	9.91	2.35						99.7											5.50	
38	Gomp no const	1.67	0.6399	9.1462							99.4											5.50	
39	Dead before age 1																						
40	Dead before age 1																						

		Equation 1										Equation 2									
		Gompertz Coefficients				Linear Regression Coefficients						Gompertz Coefficients				Linear Regression Coefficients							
Tree-id	Description	B	M	C	A	b_0	b_1	b_2	b_3	b_4	Adjusted R^2	B_1	M_1	C_1	A_1	b_0_1	b_1_1	b_2_1	b_3_1	b_4_1	Adjusted R^2	Max Age	Node
41	Dead before age 1																						
42	Dead before age 1																						
43	Gomp with const	0.4061	-12.46	4107	-4084						98.6											5.50	
44	Dead before age 1																						
45	Spline	0.987	-0.216	7.04							89.8	3.097	5.125	0.8224	6.7							5.50	3.4
46	Dead before age 1																						
47	Gomp no const	1.5712	0.7339	9.1228							99.8											5.50	
48	Dead before age 1																						
49	Dead before age 1																						
50	Gomp with const	0.322	-1	42.8	-19.6						99.9											5.50	
51	Gomp with const	1.67	1.432	5.945	4.117						99.7											5.50	
52	Spline	15.29	1.051	0.4962	3.204							0.01283	287	8.512E+15	3.433							5.50	3.4
53	Gomp no const	2.1157	0.5837	6.9902							99.7											5.50	
54	Gomp no const	3.13	0.6663	5.0215							99.3											5.50	
55	Gomp no const	2.15	0.121	3.70243							99.2											5.50	
56	Gomp no const	3.445	0.7317	5.0892							99.1											5.50	
57	2 points					2.5658	0.7209				100											1.43	
58	Spline					3										3.2						1.92	1.9
59	Gomp with const	0.1717	-24.2	1805	-1776						99.8											5.50	
60	Gomp no const	12.95	0.7976	3.6																		1.92	
61	Gomp with const	0.4785	-9.755	1744	-1729						99.8											5.50	
62	Gomp with const	1.388	1.306	5.86	3.656						99.6											5.50	
63	Dead before age 1																						
64	1 point					2					100											1.02	
65	Gomp with const	3.185	1.3091	2.31	4.615						99.8											3.41	
66	Gomp with const	1.733	1.425	4.62	4.906						99.7											5.50	
67	Gomp no const	1.409	0.5348	9.2499							98.7											5.50	
68	Dead before age 1																						
69	Gomp with const	0.543	-0.94	33.1	-18.4						99.8											5.50	
70	Gomp no const	1.003	-0.301	5.579							90.4											2.45	
71	1 point					1.2					100											1.02	
72	1 point					2.9					100											1.02	
73	Gomp no const	3.649	0.6514	5.4653							97.1											3.41	
74	Gomp no const	0.4672	1.87	22.24							99.1											5.50	
75	Gomp with const	2.055	1.106	1.87	4.14						97.8											5.50	
76	Gomp no const	0.8822	0.9922	13.3247							99.9											5.50	
77	Gomp with const	1.446	1.074	7.14	3.5						99.8											5.50	
78	Gomp no const	7.35	0.8267	4.8523							98.2											2.45	
79	Gomp with const	3.369	1.4116	1.8667	4.4571						99.7											3.41	
80	Gomp with const	0.55	-1.44	45	-29						99.8											5.50	
81	1 point					2.9					100											1.02	
82	Gomp with const	3.569	1.4187	1.3347	4.3797						99.8											3.41	

		Equation 1										Equation 2								
		Gompertz Coefficients				Linear Regression Coefficients						Gompertz Coefficients				Linear Regression Coefficients						
Tree-id	Description	B	M	C	A	b_0	b_1	b_2	b_3	b_4	Adjusted R^2	B_1	M_1	C_1	A_1	b_0_1	b_1_1	b_2_1	b_3_1	b_4_1	Adjusted R^2	Max Age	Node
83	1 point					2.2					100											1.02	
84	2 points					2.7553	0.2403				100											1.43	
85	Gomp no const	1.379	0.4387	7.7969							98.8											5.50	
86	Gomp with const	0.342	-0.6	33.8	-14						99.9											5.50	
87	Gomp with const	0.859	1.4289	10.34	2.402						100											5.50	
88	Gomp no const	13	0.8204	4.101																		1.92	
89	Gomp with const	2.073	-1.663	640.6	-633.1						99.3											5.50	
90	Gomp no const	1.118	0.5484	9.123							98.4											5.50	
91	Gomp with const	0.3826	1.24	27.31	-4.48						99.9											5.50	
92	Gomp with const	2.601	1.5012	4.371	5.09						98.4											5.01	
93	Gomp no const	11.59	0.8434	5.702							100											2.45	
94	Dead before age 1																						
95	Gomp with const	0.2418	-19.64	2968	-2942						99.8											5.50	
96	Gomp no const	13.21	0.8742	5.802																		1.92	
97	Gomp no const	13.25	0.8809	4.701																		1.92	
98	Dead before age 1																						
99	1 point					4.8					100											1.02	
100	Gomp with const	1.095	1.5099	9.826	3.843						99.9											5.50	
101	2 points					2.2732	0.2227				100											1.92	
102	Gomp no const	13.13	0.8572	5.301																		1.92	
103	Gomp with const	0.2544	-15.53	1245	-1221						99.9											5.50	
104	Gomp no const	0.397	-2.931	3.819																		1.92	
105	Gomp with const	2.223	0.952	4.13	3.06						99.7											5.50	
106	Gomp no const	1.2064	0.7002	9.2916							99.7											5.50	
107	1 point					1					100											1.02	
108	1 point					5					100											1.02	
109	Gomp with const	0.4063	-4.549	159.3	-138.1						99.9											5.50	
110	Gomp no const	1.143	0.6455	9.377							99											5.50	
111	Spline	3.249	0.519	6.0926							99.5	5.099	4.853	0.3114	6.1							5.50	3.4
112	Gomp with const	6.603	1.629	1.438	5.293						98											5.50	
113	Gomp with const	0.3156	-15.65	3670	-3646						99.7											5.50	
114	Gomp no const	1.0042	0.9046	10.523							99.5											5.50	
115	Gomp no const	1.4682	0.8908	9.829							99.6											5.50	
116	Gomp no const	3.68	0.723	4.2206							85.3											5.50	
117	Gomp with const	2.33	-1.137	381.2	-375						99.4											5.50	
118	Dead before age 1																						
119	Gomp with const	0.3148	-12.5	1284	-1261						99.9											5.50	
120	Gomp no const	0.9382	0.9867	12.685							99.6											5.50	
121	Gomp with const	1.632	1.926	7.332	5.37						99.7											5.50	
122	Gomp no const	1.686	0.8486	7.7667							99.1											5.50	
123	Gomp no const	4.106	0.7085	6.676							94.9											5.50	

		Equation 1										Equation 2								
		Gompertz Coefficients				Linear Regression Coefficients						Gompertz Coefficients				Linear Regression Coefficients						
Tree-id	Description	B	M	C	A	b_0	b_1	b_2	b_3	b_4	Adjusted R^2	B_1	M_1	C_1	A_1	b_0_1	b_1_1	b_2_1	b_3_1	b_4_1	Adjusted R^2	Max Age	Node
124	1 point					5.3					100											1.02	
125	1 point					6					100											1.02	
126	Gomp with const	2.443	1.308	5.3	3.709						99.4											5.50	
127	1 point					5					100											1.02	
128	Gomp no const	1.411	0.4985	9.173							98.9											5.50	
129	Gomp with const	1.671	1.314	5.396	3.663						99.7											5.50	
130	Dead before age 1																						
131	Gomp no const	5.867	0.8296	7.513																		1.92	
132	Gomp no const	1.62	0.4624	7.1676							98.2											5.50	
133	Gomp with const	0.3326	-16.45	5663	-5640						99.7											5.50	
134	Gomp no const	0.8641	1.1396	16.803							99.7											5.50	
135	Gomp with const	3.076	1.261	2.285	3.723						99.8											5.50	
136	Gomp no const	1.6345	0.7015	8.4751							99.5											5.50	
137	Gomp with const	2.815	1.2753	2.497	4.782						99.7											5.50	
138	Gomp no const	0.6098	1.5641	21.533							99.9											5.50	
139	Gomp with const	2.347	-1.106	266.4	-259.4						98.6											5.50	
140	Gomp no const	0.7109	1.491	21.493							99.9											5.50	
141	Dead before age 1																						
142	Gomp no const	1.9556	0.6656	7.1055							100											2.45	
143	Dead before age 1																						
144	Gomp with const	0.5823	-0.3	32.2	-15.6						99.9											5.50	
145	Gomp no const	0.9684	1.0495	11.943							99.8											5.50	
146	Gomp with const	3.1898	1.75328	1.8056	6.1945						100											5.50	
147	Gomp no const	2.197	0.502	4.709							94.3											2.45	
148	Gomp with const	1.436	1.42	8.72	3.672						99.7											5.50	
149	Gomp no const	0.7387	1.2986	17.399							99.9											5.50	
150	Gomp with const	13.74	1.318	1.1	3.9						100											3.41	
151	Gomp with const	2.618	-1.351	881.9	-876.3						99.7											4.41	
152	Gomp with const	2.135	1.167	5.12	3.7						99.6											5.50	
153	2 points					0.5105	0.4806				100											1.43	
154	Gomp no const	2.048	0.455	5.51							96.7											4.41	
155	Gomp with const	0.2658	-18.73	3073	-3053						99.8											5.50	
156	Gomp with const	0.4038	-5.197	156.9	-139.7						99.9											5.50	
157	Gomp with const	1.3864	1.2638	8.09	2.517						100											3.41	
158	Gomp no const	0.7954	1.2588	16.437							99.7											5.50	
159	Gomp no const	0.9415	0.9372	11.6011							99.9											5.50	
160	Gomp with const	0.326	-0.46	46.3	-20.3						99.9											5.50	
161	Gomp with const	2.815	0.83	6.09	0.22						99.9											5.50	
162	Gomp no const	1.0159	1.0506	12.155							99.8											5.50	
163	Gomp with const	0.4789	-13.4	16054	-16032						99.5											5.50	
164	Gomp no const	0.7163	1.3561	18.733							99.7											5.50	

		Equation 1										Equation 2								
		Gompertz Coefficients				Linear Regression Coefficients						Gompertz Coefficients				Linear Regression Coefficients						
Tree-id	Description	B	M	C	A	b_0	b_1	b_2	b_3	b_4	Adjusted R^2	B_1	M_1	C_1	A_1	b_0_1	b_1_1	b_2_1	b_3_1	b_4_1	Adjusted R^2	Max Age	Node
165	Gomp with const	0.5339	-8.098	1393	-1377						99.7											5.50	
166	Spline	4.89	0.8611	7.6312							99.3	1.819	4.892	1.115	7.7							5.50	3.4
167	Gomp no const	2.351	0.9093	10.052							96.1											2.45	
168	Gomp no const	1.0439	0.9779	12.74							99.6											5.50	
169	Gomp with const	1.342	-4.214	4183	-4174						98.2											5.50	
170	Dead before age 1																						
171	Gomp with const	0.4582	-12.83	8754	-8733						99.7											5.50	
172	Gomp no const	1.449	0.9046	11.691							99.1											5.50	
173	Gomp with const	0.3384	-13.16	2126	-2104						99.9											5.50	
174	Gomp with const	3.708	0.4475	21.77	-15.28						87.5											5.50	
175	Gomp with const	1.0662	-1.32	100	-87						100											5.50	
176	Gomp with const	0.4419	-14.49	13733	-13713						99.4											5.50	
177	Gomp no const	1.2162	1.0158	12.8446							99.8											5.50	
178	Gomp with const	0.4349	-13.96	10581	-10561						99.6											5.50	
179	Gomp no const	3.91	0.8225	7.986							94											5.50	
180	Gomp no const	1.4229	0.8476	10.0071							99.8											5.50	
181	Gomp no const	0.9685	1.1537	13.847							99.8											5.50	
182	Gomp with const	0.4206	-14.57	11155	-11135						99.5											5.50	
183	Gomp with const	5.592	1.355	3.816	1.895						100											5.50	
184	1 point					1.1					100											1.02	
185	Gomp with const	0.6728	-2.711	133	-118.6						99.9											4.41	
186	Gomp with const	0.2995	-15.18	2829	-2802						99.7											5.50	
187	Gomp no const	1.2606	1.1099	12.6272							99.9											5.50	
188	Gomp with const	0.64	-1.26	62	-46						99.8											5.50	
189	Gomp no const	1.5478	1.662	10.8286							99.7											5.50	
190	Gomp with const	0.3773	-12.94	3482	-3460						99.9											5.50	
191	Gomp with const	2.211	0.723	6.76	-1.62						99.4											5.50	
192	Gomp with const	0.4562	-10.59	2721	-2704						99.5											5.50	
193	Gomp no const	2.365	0.9576	3.5753							99.7											5.01	
194	Gomp no const	9.84	0.9475	6.2507							99.7											2.45	
195	Gomp no const	1.3865	1.073	13.3039							99.8											5.50	
196	Gomp with const	1.2709	1.4251	10.398	2.873						100											5.50	
197	Gomp no const	0.8286	1.1866	15.901							99.8											5.50	
198	Gomp with const	0.628	-0.63	57	-35						99.2											5.50	
199	Gomp with const	0.9192	-7.447	8269	-8263						92.2											5.50	
200	2 points					-4.2	9.1313				100											1.43	
201	Gomp with const	0.5187	-13.49	30167	-30148						98.3											5.50	
202	Gomp with const	0.878	1.652	14.64	2.32						99.8											5.50	
203	Polynomial 4th order					-6.0519	17.227	-7.111	1.2613	-0.0801	98.2											5.50	
204	Gomp with const	0.423	-1.43	67	-43						99.6											5.50	
205	Dead before age 1																						

		Equation 1										Equation 2								
		Gompertz Coefficients				Linear Regression Coefficients						Gompertz Coefficients				Linear Regression Coefficients						
Tree-id	Description	B	M	C	A	b_0	b_1	b_2	b_3	b_4	Adjusted R^2	B_1	M_1	C_1	A_1	b_0_1	b_1_1	b_2_1	b_3_1	b_4_1	Adjusted R^2	Max Age	Node
206	Gomp no const	1.0497	1.2716	16.912							99.5											5.50	
207	Gomp with const	0.4103	-9.006	893.7	-873.8						99.4											5.50	
208	Gomp with const	1.437	1.6988	7.264	4.152						99.7											5.50	
209	Spline					2.7868	1.6821				100	1.649	1.8282	7.382							96.4	5.50	1.4
210	Dead before age 1																						
211	Gomp no const	2.538	0.9338	12.256							96.2											5.50	
212	Dead before age 1																						
213	Gomp no const	1.2579	1.0377	11.5923							99.7											5.50	
214	Gomp no const	0.8601	1.1377	17.544							99.9											5.50	
215	2 points					0.0368	6.2477				100											1.43	
216	Gomp no const	0.4949	1.6557	26.22							99.7											5.50	
217	Gomp no const	1.7566	0.80685	8.772							100											2.45	
218	Gomp no const	1.2349	1.0632	13.2998							99.8											5.50	
219	Gomp with const	0.568	0.775	30.9	-6.7						99.9											5.50	
220	Gomp no const	1.0749	0.8696	13.114							99.7											5.50	
221	Gomp no const	1.0527	0.9812	14.2882							99.9											5.50	
222	Gomp with const	0.6896	0.603	28.97	-8.16						99.9											5.50	
223	Gomp with const	0.3334	-16.33	7082	-7054						99.6											5.50	
224	Gomp with const	0.4176	-8.842	1068	-1046						99.9											5.50	
225	Gomp no const	1.3466	0.966	11.2211							99.8											5.50	
226	Gomp with const	0.491	-0.8	53.1	-29.6						99.8											5.50	
227	Gomp with const	0.4296	-9.338	1626	-1601						99.9											5.50	
228	Gomp no const	1.32	0.6626	11.14							98.9											5.50	
229	Dead before age 1																						
230	Dead before age 1																						
231	Gomp with const	0.7255	-10.12	22150	-22137						94.1											5.50	
232	Gomp with const	0.4497	-14.18	18769	-18744						99.6											5.50	
233	Gomp with const	0.3176	-17.37	9124	-9091						99.7											5.50	
234	Gomp with const	0.6905	-10.75	39444	-39428						99.7											5.50	
235	Dead before age 1																						
236	Gomp with const	0.6605	-9.076	8551	-8534						98.8											5.50	
237	1 point					5.3					100											1.02	
238	Dead before age 1																						
239	Gomp with const	0.7344	-9.964	32473	-32458						98.4											5.50	
240	Gomp with const	0.4551	-5.89	430.4	-408.8						100											5.50	
241	Gomp no const	0.4402	1.78	26.09							99.3											5.50	
242	Gomp with const	0.491	-0.68	57.5	-32.2						99.9											5.50	
243	Gomp with const	0.9208	-7.43	22598	-22585						99.8											5.50	
244	Gomp with const	2.144	-1.505	1410	-1400						99.8											5.50	
245	Dead before age 1																						
246	Gomp with const	0.438	-0.16	58.9	-27						99.8											5.50	

		Equation 1										Equation 2								
		Gompertz Coefficients				Linear Regression Coefficients						Gompertz Coefficients				Linear Regression Coefficients						
Tree-id	Description	B	M	C	A	b_0	b_1	b_2	b_3	b_4	Adjusted R^2	B_1	M_1	C_1	A_1	b_0_1	b_1_1	b_2_1	b_3_1	b_4_1	Adjusted R^2	Max Age	Node
247	Gomp no const	1.788	0.5935	7.1704							99.4											5.50	
248	1 point					4.6					100											1.02	
249	Gomp with const	0.3398	-9.98	629.5	-609.8						99.9											5.50	
250	Gomp no const	2.056	0.168	2.261																		1.92	
251	Gomp no const	2.237	0.7011	8.011																		1.92	
252	Spline	15.29	1.051	1.365	4.037							1.442	4.939	1.72	5.4							5.50	3.4
253	Gomp no const	1.1831	0.9021	11.198							99.5											5.50	
254	Dead before age 1																						
255	Gomp with const	0.2034	-17.74	1165	-1135						99.9											5.50	
256	Straight line(no growth from age 1)					2.3																1.92	
257	Gomp with const	1.3	-4.443	3137	-3130						98.7											5.50	
258	Gomp no const	1.1987	0.8095	9.8173							99.6											5.50	
259	Gomp no const	3.98	0.6313	5.721							89.2											5.50	
260	Gomp with const	1.025	1.52	9.77	3.176						99.8											5.50	
261	Dead before age 1																						
262	Gomp with const	1.312	1.362	7.8	3.62						99.6											5.50	
263	Gomp with const	1.92	-2.038	330.4	-325						95.2											5.50	
264	Gomp no const	1.767	-0.099	5.0743							96.2											5.50	
265	Dead before age 1																						
266	Spline	2.955	0.6525	6.6026							99.5	0.01283	225.3	18917018	6.176							5.50	3.4
267	Gomp no const	3.203	0.4885	4.643							70.5											2.45	
268	Gomp with const	2.019	1.293	5.462	3.654						99.4											5.50	
269	Gomp no const	1.019	-0.631	5.0175							90.7											5.50	
270	Gomp with const	1.057	1.364	11.17	2.51						99.8											5.50	
271	Dead before age 1																						
272	Spline	2.7084	0.4713	6.02474							100	0.01283	225.3	18917018	5.376							5.50	3.4
273	Gomp no const	2.037	0.4293	5.1637							98.5											5.50	
274	Gomp no const	1.5363	0.7917	9.8684							99.5											5.50	
275	Dead before age 1																						
276	Gomp no const	1.759	0.5895	7.4271							98.4											5.50	
277	Gomp with const	1.626	1.4184	6.485	4.068						99.8											5.50	
278	1 point					2.2					100											1.02	
279	Gomp with const	2.479	0.78	5.25	0.98						99.6											5.50	
280	Dead before age 1																						
281	Dead before age 1																						
282	Gomp with const	1.177	-5.21	5853	-5843						98.4											5.50	
283	Spline					1.8						1.64	3.713	0.839	1.348						93.4	5.50	1.9
284	Gomp with const	2.141	1.28	4.327	3.656						99.2											5.50	
285	Gomp no const	2.322	0.371	5.0499							84.1											5.50	
286	Gomp with const	0.4391	-8.352	782.9	-765.8						100											5.50	
287	Gomp no const	1.698	0.6735	7.594							99.2											5.50	

		Equation 1										Equation 2								
		Gompertz Coefficients				Linear Regression Coefficients						Gompertz Coefficients				Linear Regression Coefficients						
Tree-id	Description	B	M	C	A	b_0	b_1	b_2	b_3	b_4	Adjusted R^2	B_1	M_1	C_1	A_1	b_0_1	b_1_1	b_2_1	b_3_1	b_4_1	Adjusted R^2	Max Age	Node
288	Gomp no const	4.07	0.6869	4.548							82.7											5.50	
289	Gomp with const	1.942	1.251	3.818	3.805						99.8											5.50	
290	Gomp no const	1.2556	0.7034	9.5896							99.4											5.50	
291	Gomp no const	1.1435	0.7465	10.7819							99.9											5.50	
292	1 point					2.5					100											1.02	
293	Dead before age 1																						
294	Gomp with const	0.2769	-16	2048	-2025						99.9											5.50	
295	1 point					5.5					100											1.02	
296	Dead before age 1																						
297	1 point					3.1					100											1.02	
298	Gomp with const	3.556	0.3324	14.29	-8.789						89.5											5.50	
299	Gomp no const	0.6291	1.5817	20.919							99.8											5.50	
300	Gomp no const	1.2733	0.7511	9.1781							99.7											5.50	
301	Gomp with const	1.933	-2.005	473.7	-467.8						99.1											5.50	
302	Gomp no const	1.4056	0.6559	8.1553							99.4											5.50	
303	Gomp with const	1.0666	1.225	9.76	1.8						99.9											5.50	
304	Gomp with const	16.17	1.894	0.2	5.3						100											3.41	
305	Gomp no const	13.54	0.9141	5.102																		1.92	
306	Gomp no const	4.3	0.7174	5.129																		1.92	
307	Gomp with const	1.99	1.7685	3.723	6.632						99.6											5.50	
308	2 points					3.3866	0.1114				100											1.92	
309	Gomp no const	0.5709	1.6201	24.091							99.8											5.50	
310	1 point					2.2					100											1.02	
311	1 point					1					100											1.02	
312	Gomp with const	0.2104	-12.51	316.3	-292.9						100											5.50	
313	Gomp no const	12.18	0.8847	4.502							100											2.45	
314	Gomp with const	2.692	1.3527	2.216	4.21						99.7											5.50	
315	Gomp no const	0.8434	0.8973	11.451							99.4											5.50	
316	Gomp no const	2.213	0.7557	8.745																		1.92	
317	Dead before age 1																						
318	2 points					3.5211	0.9612				100											1.43	
319	Gomp with const	1.874	-2.575	922.7	-917.5						99.6											3.41	
320	Gomp with const	3.136	1.2728	2.497	4.429						99.8											3.41	
321	Gomp with const	1.561	1.6309	4.786	4.477						99.7											5.50	
322	Gomp no const	0.343	-3.26	5.65							94.5											2.45	
323	Gomp no const	0.7162	1.1187	14.0694							100											5.50	
324	Gomp no const	2.067	0.7202	8.922																		1.92	
325	Gomp no const	13.13	0.8572	5.301																		1.92	
326	Gomp with const	2.354	1.438	1.836	4.785						97.9											5.50	
327	1 point					1.2					100											1.02	
328	Straight line(no growth from age 1)					4.8					100											1.92	

		Equation 1										Equation 2								
		Gompertz Coefficients				Linear Regression Coefficients						Gompertz Coefficients				Linear Regression Coefficients						
Tree-id	Description	B	M	C	A	b_0	b_1	b_2	b_3	b_4	Adjusted R^2	B_1	M_1	C_1	A_1	b_0_1	b_1_1	b_2_1	b_3_1	b_4_1	Adjusted R^2	Max Age	Node
329	Gomp no const	0.5562	1.5171	19.774							99.9											5.50	
330	Gomp no const	0.808	0.7952	11.98																		1.92	
331	Gomp no const	1.332	-0.216	5.577							96											3.41	
332	Gomp with const	4.872	1.35853	1.61218	4.59148						100											3.41	
333	Gomp with const	1.75219	1.38272	4.3849	3.1397						100											3.41	
334	Gomp no const	1.117	-0.433	4.9122							95.6											5.50	
335	Gomp no const	0.7917	0.6622	9.721							99.6											5.50	
336	Gomp no const	1	0.498	9.236							94.5											5.50	
337	Gomp with const	3.584	1.7408	1.5208	5.7683						98.3											5.50	
338	Gomp no const	5.345	0.7394	4.508																		1.92	
339	Gomp no const	0.9019	0.8585	12.126							99.7											5.50	
340	Spline	3.327	0.3424	4.1111							99.5	0.01283	271.4	2.722E+13	3.196							5.50	3.4
341	Gomp no const	0.5538	1.584	21.762							99.7											5.50	
342	Gomp no const	1.521	0.333	5.958							98.8											2.45	
343	Gomp no const	2.107	0.1676	4.493							98.7											5.50	
344	Gomp with const	2.6282	1.3471	3.0885	3.9106						100											5.50	
345	Gomp with const	0.5167	1.753	22.24	0.35						99.9											5.50	
346	Gomp with const	5.608	1.36	1.748	4.598						99.2											5.50	
347	1 point					3					100											1.02	
348	1 point					4					100											1.02	
349	Gomp with const	5.08	1.5997	1.0878	4.1971						97.1											5.50	
350	Gomp with const	1.397	1.651	5.313	4.679						99.5											5.50	
351	Gomp no const	0.898	0.5527	9.216							98.4											5.50	
352	Gomp no const	4.062	0.6817	5.193							96.1											5.50	
353	Gomp with const	2.001	1.839	4.746	4.722						97.9											5.50	
354	Gomp with const	1.62	1.661	3.715	5.211						96.5											5.50	
355	Dead before age 1																						
356	Gomp no const	1.4695	0.8545	9.6082							99.5											5.50	
357	Spline	15.29	1.051	0.7443	4.556							0.3772	6.921	3.81	5.311							5.50	3.4
358	Gomp with const	0.3161	-17.88	7193	-7169						99.6											5.50	
359	Gomp no const	1.379	0.267	7.2188							98.7											5.50	
360	Gomp with const	0.6423	-8.666	4207	-4194						99.5											5.50	
361	Spline	3.693	0.6804	5.3276							99.7	0.01283	158.4	8176							99.1	5.50	3.4
362	Gomp with const	1.035	0.4	18.4	-5.8						99.4											5.50	
363	Gomp with const	0.5687	-12.2	19340	-19325						99.4											5.50	
364	Gomp with const	1.382	-0.27	21	-13						98.5											5.50	
365	Gomp no const	1.0822	0.8521	11.822							99.6											5.50	
366	Gomp with const	0.4408	-8.597	792.3	-776.3						99.7											5.50	
367	Gomp no const	1.1771	0.9858	12.372							99.3											5.50	
368	Gomp with const	0.3909	-14.05	4023	-4006						99.4											5.50	
369	Gomp no const	1.665	0.6238	8.7383							99.2											5.50	

		Equation 1										Equation 2									
		Gompertz Coefficients				Linear Regression Coefficients						Gompertz Coefficients				Linear Regression Coefficients							
Tree-id	Description	B	M	C	A	b_0	b_1	b_2	b_3	b_4	Adjusted R^2	B_1	M_1	C_1	A_1	b_0_1	b_1_1	b_2_1	b_3_1	b_4_1	Adjusted R^2	Max Age	Node
370	Dead before age 1																						
371	Gomp with const	0.2629	-17.59	2579	-2555						99.6											5.50	
372	Gomp no const	1.248	0.8626	10.126							99.1											5.50	
373	Dead before age 1																						
374	Gomp no const	1.246	0.034	7.314							93.8											5.50	
375	Gomp with const	0.3638	-16.05	8100	-8079						98.8											5.50	
376	Gomp with const	0.405	-12.04	3270	-3248						99.8											5.50	
377	Gomp with const	1.635	1.403	5.473	3.886						99.5											5.50	
378	1 point					4.7					100											1.02	
379	Gomp no const	1.1785	1.0864	11.324							99.6											5.50	
380	1 point					4.5					100											1.02	
381	Gomp no const	2.17	0.8265	9.666																		1.92	
382	Gomp with const	0.4474	-13.44	7573	-7557						99.6											5.50	
383	Gomp with const	1.032	1.425	9.57	2.66						99.7											5.50	
384	Gomp no const	13.85	0.9364	6.203																		1.92	
385	Spline	3.249	0.7512	4.8753							98.8	0.01283	296.1	4.517E+17	4.758							5.50	3.4
386	Gomp no const	4.53	0.696	5.68							95.5											3.41	
387	Gomp with const	0.225	-21.1	3310	-3281						96.6											5.50	
388	Spline	2.553	0.5747	5.1132							99	1.641	4.462	0.6029	5.098							5.50	3.4
389	Gomp no const	1.0681	0.9315	12.7577							99.9											5.50	
390	Gomp with const	0.3531	-14.87	3175	-3159						99.8											5.50	
391	Gomp with const	0.2757	-19.32	4956	-4932						99.7											5.50	
392	Gomp with const	1.825	1.4823	4.659	4.365						99.7											5.50	
393	Gomp with const	0.8082	1.693	15.97	2.81						99.9											5.50	
394	Dead before age 1																						
395	Gomp no const	1.2144	0.9791	11.177							99.9											5.50	
396	Gomp with const	1.968	-1.914	397.8	-390.9						96.8											5.50	
397	Gomp with const	0.5612	-12.18	17229	-17213						98.3											5.50	
398	Gomp with const	0.3322	-9.14	624.9	-599						99.7											5.50	
399	Gomp with const	0.611	-1.25	47	-32						99.8											5.50	
400	Gomp no const	0.931	1.1486	14.045							98.7											5.50	
401	Gomp with const	1.45	1.462	6.859	4.223						99.5											5.50	
402	Gomp with const	1.115	-5.656	1284	-1279						85.5											5.50	
403	Dead before age 1																						
404	Gomp no const	5.792	0.80891	7.80629							100											2.45	
405	Gomp with const	1.3002	1.402	11.614	2.777						99.9											5.50	
406	Gomp with const	2.698	1.2	2.275	4.257						99.4											3.41	
407	2 points					3.2763	1.2015				100											1.43	
408	Gomp no const	1.4155	0.7507	9.5575							99.9											5.50	
409	Gomp no const	4.079	0.8196	7.485																		1.92	
410	Spline	6.3286	0.75896	7.4024							100	0.01283	124.5	838.4							93.3	5.50	3.4

		Equation 1										Equation 2								
		Gompertz Coefficients				Linear Regression Coefficients						Gompertz Coefficients				Linear Regression Coefficients						
Tree-id	Description	B	M	C	A	b_0	b_1	b_2	b_3	b_4	Adjusted R^2	B_1	M_1	C_1	A_1	b_0_1	b_1_1	b_2_1	b_3_1	b_4_1	Adjusted R^2	Max Age	Node
411	Gomp with const	0.4753	-9.52	1782	-1764						99.4											5.50	
412	Dead before age 1																						
413	Gomp with const	0.98	0.679	20.77	-5.03						99.9											5.50	
414	Polynomial 3rd order					-5.237	12.709	-2.61	0.1969		99.9											5.50	
415	Gomp with const	0.2889	-16.03	3159	-3131						99.9											5.50	
416	Gomp with const	0.4113	-12.58	3976	-3956						99.8											5.50	
417	Gomp no const	0.9356	1.0793	15.957							99.8											5.50	
418	Dead before age 1																						
419	Gomp no const	0.8449	1.1354	16.486							99.4											5.50	
420	Gomp with const	1.338	-4.236	5856	-5845						99.1											5.50	
421	Gomp with const	0.7435	-9.813	32247	-32232						99.6											5.50	
422	Gomp no const	1.5136	0.7145	10.722							99.8											5.50	
423	Spline	4.15	0.8053	7.262							95.5	0.01283	281.4	5.872E+14	7.223							5.50	3.4
424	Spline	3.634	0.7903	2.3192							99.6	0.6101	2.7396	4.467							99.8	5.50	3.4
425	Gomp with const	2.899	-3.021	147.8	-139.5						97.3											5.50	
426	Gomp no const	1.0164	1.2193	15.587							99.7											5.50	
427	Gomp no const	13.6	0.9198	6.103																		1.92	
428	Gomp with const	1.2923	1.4114	8.427	4.002						100											5.50	
429	Gomp with const	0.6627	-10.97	25766	-25752						99.7											5.50	
430	Gomp with const	0.5143	-9.62	2953	-2935						99.7											5.50	
431	Gomp no const	0.936	1.01	13.844							99.8											5.50	
432	Gomp no const	14.04	0.9466	8.204																		1.92	
433	Gomp with const	0.2632	-21.43	7590	-7564						99.2											5.50	
434	Gomp with const	1.0996	1.218	10.73	2.01						99.9											5.50	
435	Gomp no const	13.44	0.905	4.102																		1.92	
436	Gomp with const	0.3278	-15.72	5533	-5504						99.8											5.50	
437	Gomp with const	1.3927	1.1867	9.276	1.29						100											5.50	
438	Gomp with const	1.2575	1.476	10.862	2.699						99.9											5.50	
439	Gomp with const	3.484	1.4118	3.6855	4.7295						99.9											5.50	
440	Gomp with const	0.4433	-0.98	50.4	-27.9						99.9											5.50	
441	Gomp with const	0.5257	-7.992	1550	-1532						99.9											5.50	
442	Gomp with const	2.885	1.319	3.987	3.434						99.7											5.50	
443	Gomp no const	0.8518	1.139	17.36							99.9											5.50	
444	Gomp no const	1.576	0.5095	8.4891							99.3											5.50	
445	Gomp with const	0.5203	-11.04	8235	-8215						99.9											5.50	
446	Gomp with const	0.38	-15.33	9972	-9947						99.6											5.50	
447	Gomp with const	0.902	-1.9	152	-136						99.6											5.50	
448	Gomp with const	0.889	-7.791	18424	-18413						97.4											5.50	
449	Gomp no const	2.125	0.8936	10.98																		1.92	
450	Gomp with const	4.962	1.393	5.868	5.842						98.8											5.50	
451	Gomp with const	1.029	-1.5	125	-111						99.6											5.50	

		Equation 1										Equation 2								
		Gompertz Coefficients				Linear Regression Coefficients						Gompertz Coefficients				Linear Regression Coefficients						
Tree-id	Description	B	M	C	A	b_0	b_1	b_2	b_3	b_4	Adjusted R^2	B_1	M_1	C_1	A_1	b_0_1	b_1_1	b_2_1	b_3_1	b_4_1	Adjusted R^2	Max Age	Node
452	Gomp with const	0.3618	-14.69	6049	-6024						99.5											5.50	
453	Gomp no const	1.641	0.765	11.05							92.5											5.50	
454	Dead before age 1																						
455	Gomp with const	0.4896	-8.997	2134	-2114						99.8											5.50	
456	Gomp with const	2.401	-1.013	711.1	-700.7						99.5											5.50	
457	Gomp no const	1.0942	1.3082	13.948							99.5											5.50	
458	fell at 1.4					3.9						5.99	1.4331	4.314							95.7	3.41	1.4
459	Gomp with const	0.4052	-15.77	16107	-16083						99.3											5.50	
460	2 points					1					100											1.43	
461	Gomp no const	0.5217	1.4069	25.658							99.7											5.50	
462	Gomp no const	5.138	0.81881	5.00874							100											2.45	
463	Spline	3.214	-1.345	5624	-5617							0.01283	311.7	1.67E+22	7.493							5.50	3.4
464	Gomp with const	0.7613	0.554	27.04	-7.54						99.9											5.50	
465	fell at 1.4					3.9						1.339	1.102	4.2							89.1	5.50	1.4
466	Gomp with const	0.3355	-13.26	2638	-2610						99.8											5.50	
467	Gomp no const	1.431	0.9447	12.777							98.9											5.50	
468	Gomp with const	0.4112	-10.89	2655	-2629						99.7											5.50	
469	Gomp with const	1.094	0.361	21.5	-8.2						99.9											5.50	
470	Gomp with const	0.3864	-16.05	14310	-14284						99.3											5.50	
471	Gomp no const	2.474	0.8078	7.0559							99.8											3.41	
472	Gomp no const	1.0702	1.1365	16.273							99.8											5.50	
473	Gomp no const	2.828	0.6888	6.387							98.4											2.45	
474	Gomp with const	0.422	-14.48	12943	-12919						99.5											5.50	
475	Gomp with const	0.8664	-8.062	23664	-23653						99.1											5.50	
476	Gomp with const	0.3382	-14.62	4810	-4780						99.9											5.50	
477	Gomp with const	0.4298	-14.4	13367	-13344						99.3											5.50	
478	Gomp no const	1.952	1.045	14.04																		1.92	
479	Gomp no const	1.4584	0.9615	13.348							99.8											5.50	
480	Gomp with const	0.3705	-9.889	1018	-994.6						99.9											5.50	
481	Dead before age 1																						
482	Gomp with const	0.3275	-17.96	12666	-12635						99.2											5.50	
483	Gomp with const	0.5738	-8.769	3562	-3544						99.8											5.50	
484	Gomp no const	1.38	1.1407	13.816							99.2											5.50	
485	Gomp with const	0.379	-2.8	96	-71						99.8											5.50	
486	Gomp with const	0.2929	-7.915	380.1	-348.3						99.9											5.50	
487	Gomp with const	0.3084	-15.83	4763	-4731						99.7											5.50	
488	Dead before age 1																						
489	Gomp with const	0.611	-8.835	6122	-6102						99.7											5.50	
490	Gomp with const	4.324	0.8308	7.152	-0.3342						94.3											5.50	
491	Gomp with const	1.3745	1.271	14.79	2.32						99.9											5.50	
492	Dead before age 1																						

		Equation 1										Equation 2								
		Gompertz Coefficients				Linear Regression Coefficients						Gompertz Coefficients				Linear Regression Coefficients						
Tree-id	Description	B	M	C	A	b_0	b_1	b_2	b_3	b_4	Adjusted R^2	B_1	M_1	C_1	A_1	b_0_1	b_1_1	b_2_1	b_3_1	b_4_1	Adjusted R^2	Max Age	Node
493	Gomp no const	1.0817	0.8068	10.3315							99.7											5.60	
494	Spline	1.986	0.031	3.9181							97.5	0.3772	6.921	1.905	3.956							5.60	3.4
495	Spline	4.84	0.7318	5.2632							98.8	0.3772	6.921	1.905	5.356							5.60	3.4
496	Dead before age 1																						
497	Dead before age 1																						
498	Gomp no const	0.9773	0.9452	11.15171							99.8											5.60	
499	Gomp with const	5.8	1.5139	0.9829	3.1995						95.9											5.60	
500	Gomp no const	0.6242	1.1389	13.558							99.8											5.60	
501	Gomp no const	0.9	0.642	10.356							98.1											5.60	
502	Gomp no const	1.2195	0.7616	9.0499							99.4											5.60	
503	Gomp no const	1.412	0.5224	7.0349							99.3											5.60	
504	Gomp with const	2.355	1.403	2.968	4.563						98.2											5.60	
505	Gomp with const	2.229	1.37	0.965	4.192						97.7											5.60	
506	Gomp with const	2.188	-1.412	135.5	-131						91.3											5.60	
507	Gomp with const	0.3433	-4.734	130.4	-109						99.8											5.60	
508	Dead before age 1																						
509	Gomp no const	2.835	0.644	7.3937							93.8											5.60	
510	Gomp no const	13.5	0.9103	5.802																		1.92	
511	Gomp no const	1.619	0.1954	5.6029							99.5											5.60	
512	Spline	2.577	0.5237	5.9491							99.9	0.8508	5.856	3.108	6.099							5.60	3.4
513	Dead before age 1																						
514	Polynomial 4th order					4.349	-0.519	0.383	-0.096	0.0083	96.09											5.60	
515	Gomp no const	0.7634	1.2308	17.305							99.4											5.60	
516	Gomp with const	2.841	1.4443	2.398	4.021						99.4											5.60	
517	Gomp no const	1.581	0.6236	8.53							98.9											5.60	
518	Gomp with const	3.92	1.184	1.484	4.481						98.6											5.60	
519	Gomp with const	0.407	-1.04	45.6	-24.3						99.9											5.60	
520	Dead before age 1																						
521	Dead before age 1																						
522	fell at 1.4					2.5						0.735	3.617	3.077	1.1756						99.6	5.60	1.4
523	2 points					0.7947	4.3253				100											1.43	
524	Gomp with const	1.573	1.464	3.465	4.869						98.7											5.60	
525	Dead before age 1																						
526	1 point					2.2					100											1.02	
527	Gomp no const	1.1006	0.5344	10.1187							99.4											5.60	
528	Spline	8.275	0.6956	4.604							99.6	0.01283	107.4	209.1							96.8	5.60	3.4
529	Spline	15.29	1.051	0.4962	2.804							1.641	4.462	0.6029	3.398							5.60	3.4
530	Gomp no const	1.1167	0.7584	10.1246							99.6											5.60	
531	Gomp with const	1.305	-4.416	4725	-4716						99.5											5.60	
532	Dead before age 1																						
533	Spline	1.685	0.07	5.274							97.8	0.106	0.03	10.66							99.6	5.60	3.4

		Equation 1										Equation 2								
		Gompertz Coefficients				Linear Regression Coefficients						Gompertz Coefficients				Linear Regression Coefficients						
Tree-id	Description	B	M	C	A	b_0	b_1	b_2	b_3	b_4	Adjusted R^2	B_1	M_1	C_1	A_1	b_0_1	b_1_1	b_2_1	b_3_1	b_4_1	Adjusted R^2	Max Age	Node
534	Gomp with const	0.8936	1.352	10.93	2.163						100											5.60	
535	Spline	5.43	0.72547	4.90375							100	3.097	5.125	0.4112	5							5.60	
536	Gomp with const	1.304	1.661	6.64	4.14						98.2											5.60	
537	Gomp no const	1.3804	0.6867	9.4134							99.9											5.60	
538	Gomp with const	1.73	-2.599	990.3	-984.4						99.8											5.60	
539	Gomp with const	0.2564	-14.87	1092	-1068						99.7											5.60	
540	Dead before age 1																						
541	Gomp with const	2.0755	1.0885	3.659	3.049						100											5.60	
542	Gomp no const	0.909	0.5934	10.347							98.6											5.60	
543	Dead before age 1																						
544	Gomp with const	1.139	-5.479	6891	-6882						99.5											5.60	
545	Gomp no const	2.294	0.6212	6.2879							99.6											5.60	
546	Gomp no const	0.42	-2.99	4.837							83.6											5.60	
547	Gomp with const	1.449	1.297	5.587	2.868						99.8											5.50	
548	Gomp with const	1.076	1.609	6.013	5.041						99.5											5.50	
549	Gomp with const	5.637	1.37	0.6049	3.9						99.7											5.50	
550	Gomp with const	1.298	1.531	8.58	3.64						99.2											5.50	
551	Gomp with const	1.257	1.191	6.37	3.16						99.8											5.50	
552	Gomp with const	3.011	-5.075	117.4	-112.5						97.3											5.01	
553	Straight line(no growth from age 1)					3.6					100											1.92	
554	Gomp no const	13.09	0.8488	3.901																		1.92	
555	Gomp with const	1.741	0.415	7.14	0.17						100											5.50	
556	Gomp with const	0.1889	-22.96	2591	-2557						99.8											5.50	
557	Gomp no const	1.873	0.221	5.1298							95.1											5.50	
558	2 points					2.6553	0.2403				100											1.43	
559	Gomp no const	1.017	0.7802	9.863																		1.92	
560	Gomp no const	3.011	0.594	6.0756							99.4											3.41	
561	2 points					3.6					100											1.43	
562	Gomp no const	0.801	0.311	8.98							96.7											5.50	
563	Gomp no const	1.1488	0.4112	8.0696							99.3											5.50	
564	Dead before age 1																						
565	Gomp no const	0.7417	0.9153	12.9702							100											5.50	
566	Gomp no const	3.388	0.4979	2.6108							99.5											2.45	
567	Gomp no const	0.9932	0.88962	13.1769							100											5.50	
568	Gomp no const	2.269	0.5058	6.5576							99.5											5.50	
569	Gomp with const	9.708	1.016	0.9699	4.934						99.7											3.41	
570	Dead before age 1																						
571	1 point					1.2																1.02	
572	Gomp with const	0.3144	-12.65	1328	-1305						99.9											5.50	
573	Gomp with const	2.323	1.613	1.1269	4.3723						99.4											5.50	
574	Gomp no const	5.007	0.7	4.41																		1.92	

		Equation 1										Equation 2								
		Gompertz Coefficients				Linear Regression Coefficients						Gompertz Coefficients				Linear Regression Coefficients						
Tree-id	Description	B	M	C	A	b_0	b_1	b_2	b_3	b_4	Adjusted R^2	B_1	M_1	C_1	A_1	b_0_1	b_1_1	b_2_1	b_3_1	b_4_1	Adjusted R^2	Max Age	Node
575	1 point					2.9					100											1.02	
576	Gomp with const	0.2733	-17.1	2688	-2664						99.8											5.50	
577	Gomp no const	1.084	0.09569	5.056																		1.92	
578	Gomp no const	0.7454	0.5988	10.339							99.7											5.50	
579	Gomp no const	5.111	0.682	4.90439							100											2.45	
580	1 point					1					100											1.02	
581	Dead before age 1																						
582	Gomp with const	1.49	1.4906	5.424	4.401						99.8											5.50	
583	Gomp with const	2.629	1.3143	3.484	3.607						99.7											5.50	
584	Gomp no const	1.679	0.6532	8.5183							99.7											5.50	
585	1 point					2					100											1.02	
586	1 point					3.6					100											1.02	
587	Gomp with const	0.3189	-13.23	1493	-1472						99.9											5.50	
588	Gomp no const	1.172	0.421	7.601							97.2											5.50	
589	Gomp with const	2.426	-0.9702	161.5	-156.3						95.2											5.50	
590	3 points					4.1024	0.3416				78.6											1.92	
591	Gomp with const	0.2988	-13.06	1423	-1396						99.7											5.50	
592	Gomp no const	1.495	0.4578	6.5622							99.3											5.50	
593	Gomp no const	1.1509	0.8574	10.6286							99.6											5.50	
594	Gomp no const	1.644	0.153	5.7671							97.8											5.01	
595	Gomp no const	10.29	0.7355	3.801							99.9											2.45	
596	2 points					2.9553	0.2403				100											1.43	
597	Gomp with const	1.702	1.313	5.112	3.223						99.8											5.50	
598	Gomp with const	2.8459	2.03509	0.40887	4.099215						100											3.41	
599	Gomp no const	0.5405	1.3529	16.777							99.9											5.50	
600	1 point					3.1					100											1.02	
601	Gomp no const	1.2027	0.6745	10.6862							100											3.41	
602	Gomp with const	0.3662	-7.587	451.2	-426.8						99.8											5.50	
603	Spline					2.2						0.009079	404.9	3.347E+16	1.637							5.50	2.5
604	Gomp no const	1.26	0.6266	10.1565							99.2											5.50	
605	Gomp no const	1.73	0.4682	6.346							97.6											5.50	
606	Gomp with const	0.3098	-13.83	2062	-2035						99.6											5.50	
607	Dead before age 1																						
608	Dead before age 1																						
609	Gomp no const	1.249	0.61	11.212							98.1											5.50	
610	Gomp with const	1.181	1.691	9.68	4.33						98.2											5.50	
611	Gomp no const	1.551	0.389	6.748							92.5											5.50	
612	Gomp no const	1.278	0.933	9.915							98.9											5.50	
613	Gomp with const	2.91	-0.2899	86.79	-79.76						91.6											5.50	
614	Gomp with const	3.332	0.1442	27.39	-21.23						89.6											5.50	
615	Gomp with const	0.502	-2.87	105	-86						99.9											5.50	

		Equation 1										Equation 2								
		Gompertz Coefficients				Linear Regression Coefficients						Gompertz Coefficients				Linear Regression Coefficients						
Tree-id	Description	B	M	C	A	b_0	b_1	b_2	b_3	b_4	Adjusted R^2	B_1	M_1	C_1	A_1	b_0_1	b_1_1	b_2_1	b_3_1	b_4_1	Adjusted R^2	Max Age	Node
616	Gomp no const	0.907	-0.795	7.386							79.5											5.50	
617	Gomp with const	0.4252	-8.703	939.9	-920.5						99.9											5.50	
618	Gomp with const	1.607	1.262	7.946	3.207						99.9											5.50	
619	1 point					4.1																1.02	
620	Gomp no const	4.12	0.7167	6.02							88.7											5.50	
621	Gomp with const	0.4384	-12.91	6722	-6702						99.5											5.50	
622	2 points					-1.1632	6.2477				100											1.43	
623	Gomp no const	1.011	-0.338	7.564							91.6											5.50	
624	1 point					5.3					100											1.02	
625	1 point					5					100											1.02	
626	1 point					5.6					100											1.02	
627	Gomp with const	1.246	1.372	8.14	3.42						99.6											5.50	
628	Dead before age 1																						
629	Gomp with const	0.8359	1.7856	14.111	3.859						100											5.50	
630	Gomp with const	4.324	1.032	4.089	3.214						97.6											5.50	
631	Gomp no const	0.8627	1.0066	15.8587							100											5.50	
632	Gomp with const	2.254	0.73	7.35	0.24						99.3											5.50	
633	Gomp no const	2.871	0.667	6.9133							99.9											3.41	
634	Gomp no const	0.794	1.238	16.418							99.2											5.50	
635	Gomp no const	1.95	0.382	5.4771							93.8											5.50	
636	Gomp no const	0.9717	1.1941	16.807							99.6											5.50	
637	Gomp with const	0.438	-1.29	56	-33						99.8											5.50	
638	Gomp no const	13.14	0.8605	3.401																		1.92	
639	Gomp with const	2.0738	1.2621	3.595	5.015						100											5.50	
640	Gomp no const	0.612	1.409	18.16							96.8											5.50	
641	Gomp no const	13.37	0.8966	4.502																		1.92	
642	Gomp no const	3.96	0.6067	5.7159							99.8											2.45	
643	Gomp no const	0.6837	1.3126	22.035							99.9											5.50	
644	Gomp no const	1.3394	0.16506	6.60238							100											2.45	
645	Gomp no const	1.19	1.0008	14.2373							99.8											5.50	
646	Gomp no const	2.013	0.606	6.9665							99											3.41	
647	Gomp with const	0.3081	-10.52	750.9	-724.7						99.9											5.50	
648	1 point					1					100											1.02	
649	Gomp with const	2.4526	1.3289	3.7479	3.7609						100											5.50	
650	Gomp no const	0.8599	1.2617	16.521							99.7											5.50	
651	Gomp no const	13.59	0.9189	6.603																		1.92	
652	Gomp with const	1.628	0.5111	13.73	-4.456						99.2											5.50	
653	Gomp no const	13.15	0.8615	4.201																		1.92	
654	Gomp no const	0.808	1.0572	15.338							99.8											5.50	
655	Gomp no const	0.8166	1.2871	17.621							99.7											5.50	
656	Gomp with const	0.4764	-8.722	1066	-1050						99.7											5.50	

		Equation 1										Equation 2								
		Gompertz Coefficients				Linear Regression Coefficients						Gompertz Coefficients				Linear Regression Coefficients						
Tree-id	Description	B	M	C	A	b_0	b_1	b_2	b_3	b_4	Adjusted R^2	B_1	M_1	C_1	A_1	b_0_1	b_1_1	b_2_1	b_3_1	b_4_1	Adjusted R^2	Max Age	Node
657	Gomp no const	1.069	0.4183	10.536							98.6											5.50	
658	Gomp with const	2.4	1.301	8.12	4.97						99.3											5.50	
659	1 point					5.7					100											1.02	
660	Gomp with const	0.4491	-12.15	5092	-5073						99.8											5.50	
661	Gomp no const	2.566	0.4639	7.9208							97.3											5.50	
662	Gomp with const	0.7296	0.595	21.58	-4.86						100											5.50	
663	Gomp with const	1.345	-4.2	3445	-3436						96.8											5.50	
664	Gomp with const	0.3984	-14.01	6672	-6650						99.6											5.50	
665	Gomp with const	0.3441	-15.52	5787	-5761						99.7											5.50	
666	Gomp no const	1.3017	0.8353	8.3377							99.5											5.50	
667	Gomp with const	0.9346	0.65	18.46	-4.07						100											5.50	
668	Gomp with const	0.4233	-13.97	8195	-8175						99.6											5.50	
669	Gomp no const	0.9859	0.9041	14.561							99.7											5.50	
670	Gomp with const	1.1407	1.609	12.971	4.026						99.8											5.50	
671	Gomp no const	1.244	0.244	8.4447							97.8											5.50	
672	Gomp no const	2.629	0.6787	9.0948							98.2											5.50	
673	1 point					5					100											1.02	
674	Gomp with const	0.2977	-12.82	1428	-1399						99.9											5.50	
675	Gomp with const	0.448	-1.1	47.5	-26.6						99.8											5.50	
676	Gomp no const	2.301	0.6398	10.33																		1.92	
677	1 point					1.2					100											1.02	
678	Gomp with const	3.41	1.2794	4.713	5.087						99.8											5.50	
679	Gomp with const	1.4005	1.3102	9.685	3.363						100											5.50	
680	Gomp with const	0.352	-1.33	54.2	-28.7						99.9											5.50	
681	1 point					1.5					100											1.02	
682	Gomp no const	0.885	0.406	11.323							95.4											5.50	
683	Gomp with const	0.4314	-1.35	72	-43.8						100											5.50	
684	2 points					2.7526	2.403				100											1.43	
685	Gomp no const	12.86	0.7272	4.3																		1.92	
686	Gomp with const	0.888	2.226	10.36	6.118						99.2											5.50	
687	Gomp with const	1.62	1.2601	8.308	3.603						100											5.50	
688	Gomp with const	1.0728	1.5669	11.757	3.169						100											5.50	
689	Gomp no const	5.095	0.769	6.619																		1.92	
690	Gomp no const	0.693	1.4098	24.022							99.6											5.50	
691	Dead before age 1																						
692	Dead before age 1																						
693	Gomp no const	0.934	0.9758	14.224							98.8											5.50	
694	fell at 1.4					5.5						0.2472	-15.92	551.2	-541.9						100	5.50	1.4
695	Gomp no const	0.9682	1.0888	15.396							99											5.50	
696	fell at 1.4					4.2						1.484	1.5786	9.26							99.5	5.50	1.4
697	Dead before age 1																						

		Equation 1										Equation 2								
		Gompertz Coefficients				Linear Regression Coefficients						Gompertz Coefficients				Linear Regression Coefficients						
Tree-id	Description	B	M	C	A	b_0	b_1	b_2	b_3	b_4	Adjusted R^2	B_1	M_1	C_1	A_1	b_0_1	b_1_1	b_2_1	b_3_1	b_4_1	Adjusted R^2	Max Age	Node
698	Gomp with const	0.7779	-9.269	38969	-38951						98.9											5.50	
699	1 point						7.3				100											1.02	
700	Dead before age 1																						
701	Gomp with const	0.4667	-12.53	8831	-8810						99.8											5.50	
702	Gomp with const	0.6676	-8.1	6188	-6169						99.6											5.50	
703	Gomp no const	2.223	0.62	8.868							95.3											2.45	
704	Gomp with const	0.3911	-12.91	4462	-4437						99.9											5.50	
705	Gomp with const	0.3493	-13.48	3422	-3394						99.9											5.50	
706	Gomp no const	4.4	0.8236	3.065							95.5											4.41	
707	Spline	7.9538	0.868111	9.20109							100	13.35	4.551	1.102	9.499							5.50	3.4
708	2 points					1.2763	1.2015				100											1.43	
709	2 points					0.7658	0.7209				100											1.43	
710	Gomp with const	0.4418	-12.91	6691	-6670						99.6											5.50	
711	Dead before age 1																						
712	Gomp with const	0.9269	1.431	15.12	1.4						99.9											5.50	
713	Gomp no const	0.6411	1.3734	24.074							99.2											5.50	
714	Gomp with const	0.3322	-6.506	261.8	-234						99.8											5.50	
715	Gomp no const	1.251	0.8781	11.742							99.5											5.50	
716	Gomp with const	1.2129	1.295	11.193	2.748						99.9											5.50	
717	Gomp no const	1.6357	0.7966	11.4039							99.9											5.50	
718	Gomp no const	0.7982	1.2555	18.9							99.9											5.50	
719	Gomp no const	1.779	0.6901	10.4459							99.5											5.50	
720	Gomp with const	0.596	-6.709	946.2	-931.5						99.9											5.50	
721	Gomp with const	0.4735	-12.54	10928	-10905						99.7											5.50	
722	Dead before age 1																						
723	Gomp with const	0.704	-1.57	107	-86						99.8											5.50	
724	Dead before age 1																						
725	Dead before age 1																						
726	Gomp no const	1.179	1.0123	11.28							97.2											5.50	
727	Gomp with const	0.4163	-14.59	10467	-10445						99.5											5.50	
728	Gomp with const	0.5702	-10.83	12621	-12602						99.8											5.50	
729	Gomp with const	0.4658	-12.25	7234	-7214						99.9											5.50	
730	Gomp with const	0.4959	-12.64	14972	-14953						99.7											5.50	
731	Gomp with const	0.5061	-10.88	5755	-5736						99.3											5.50	
732	Dead before age 1																						
733	Gomp no const	0.7887	1.4626	19.652							99.5											5.50	
734	Gomp with const	0.933	0.904	28.99	-7.84						99.8											5.50	
735	Gomp with const	0.997	0.368	20.7	-9.2						99.8											5.50	
736	Gomp with const	0.682	0.65	31.8	-9.3						99.7											5.50	
737	Gomp no const	2.275	1.0679	8.1137							99.6											5.50	
738	Gomp with const	0.4518	-12.52	7472	-7450						99.7											5.50	

		Equation 1										Equation 2								
		Gompertz Coefficients				Linear Regression Coefficients						Gompertz Coefficients				Linear Regression Coefficients						
Tree-id	Description	B	M	C	A	b_0	b_1	b_2	b_3	b_4	Adjusted R^2	B_1	M_1	C_1	A_1	b_0_1	b_1_1	b_2_1	b_3_1	b_4_1	Adjusted R^2	Max Age	Node
985	Gomp with const	1.5517	1.5216	7.857	3.833						99.9											5.50	
986	Dead before age 1																						
987	Dead before age 1																						
988	Spline	15.29	1.051	1.613	4.689							0.01283	302.9	5.518E+19	5.885							5.50	3.4
989	1 point					4.6					100											1.02	
990	Dead before age 1																						
991	Spline	15.29	1.051	0.4962	4.104							0.5934	-9.258	713.8	-708.8							5.50	3.4
992	Dead before age 1																						
993	Gomp with const	0.2536	-17.51	2362	-2335						99.9											5.50	
994	Dead before age 1																						
995	Gomp no const	1.4536	0.6648	8.7125							99.5											5.50	
996	Gomp no const	1.747	0.6672	7.8433							97.7											5.50	
997	Dead before age 1																						
998	Spline	4.813	0.6953	3.70511							100	0.215	-0.604	5.64							99.2	5.50	3.4
999	Dead before age 1																						
1000	Gomp with const	1.307	1.269	7.65	3.31						99.8											5.50	
1001	Dead before age 1																						
1002	Gomp with const	1.063	1.343	10.83	2.41						99.8											5.50	
1003	Gomp with const	1.308	1.316	8.39	2.22						99.8											5.50	
1004	Spline	16.19	1.31	0.8	3.4							0.3772	6.921	1.905	4.356							5.50	3.4
1005	Gomp with const	1.666	-2.797	1580	-1574						99.9											3.41	
1006	Gomp with const	1.855	1.379	5.857	3.996						99.1											5.50	
1007	Dead before age 1																						
1008	Gomp no const	1.296	-0.059	6.2254							95											5.50	
1009	1 point					5.4					100											1.02	
1010	Dead before age 1																						
1011	Gomp with const	1.527	1.467	7.472	4.098						99.8											5.50	
1012	Dead before age 1																						
1013	Gomp with const	1.799	-2.381	560.9	-554.4						98.3											5.50	
1014	Dead before age 1																						
1015	Gomp with const	2.815	-0.4051	37.52	-33.24						96.6											5.50	
1016	Gomp with const	0.3834	-14.2	4133	-4115						99.8											5.50	
1017	Gomp with const	1.031	1.323	8.51	2.98						99.8											5.50	
1018	Gomp with const	1.348	-4.184	4483	-4474						99.5											5.50	
1019	Gomp with const	1.948	-1.965	589.7	-583.7						98.5											5.50	
1020	Gomp no const	0.9921	1.0405	13.007							99.7											5.50	
1021	Gomp no const	3.788	0.5044	4.634							92											5.50	
1022	Gomp with const	1.714	1.207	5.51	3.23						99.6											5.50	
1023	Gomp with const	4.7	1.263	2.177	4.507						97.9											5.50	
1024	Dead before age 1																						
1025	Dead before age 1																						

		Equation 1										Equation 2								
		Gompertz Coefficients				Linear Regression Coefficients						Gompertz Coefficients				Linear Regression Coefficients							
Tree-id	Description	B	M	C	A	b_0	b_1	b_2	b_3	b_4	Adjusted R^2	B_1	M_1	C_1	A_1	b_0_1	b_1_1	b_2_1	b_3_1	b_4_1	Adjusted R^2	Max Age	Node
1026	Gomp with const	0.3289	-14.05	2375	-2353						99.7											5.50	
1027	Gomp with const	3.143	-0.03653	50.12	-44.63						98.4											5.50	
1028	Gomp no const	1.2902	0.7921	9.9098							99.3											5.50	
1029	Spline	15.29	1.051	0.7443	3.256							14.57	4.414	0.3	4.1							5.50	2.5
1030	Gomp with const	1.781	-1.551	259.9	-253.3						99.7											5.50	
1031	Gomp no const	2.59	0.6481	5.6041							98.6											5.50	
1032	Gomp no const	1.213	0.7509	10.064							99											5.50	
1033	Spline	4.762	0.6368	4.70523							100	0.4511	0.146	5.911							99.8	5.50	3.4
1034	Gomp with const	0.4643	-11.51	3852	-3836						99.5											5.50	
1035	Spline	4.774	0.6528	4.4052							100	0.01283	168.4	11410	1.565							5.50	3.4
1036	Spline	4.52	0.691	6.279							89.4					6.4						5.01	3.4
1037	Dead before age 1																						
1038	Dead before age 1																						
1039	Gomp with const	2.803	1.509	1.1175	4.1776						99.8											3.41	
1040	Gomp no const	0.6764	0.9462	14.065							99.7											5.50	
1041	Gomp no const	1.935	0.388	5.631							98.6											2.45	
1042	Gomp with const	0.8889	1.372	11.27	2.158						99.9											5.50	
1043	Gomp with const	18.39	1.43	0.5	3.8																	2.45	
1044	Gomp no const	11.87	0.8633	4.102							100											2.45	
1045	Gomp with const	0.603	2.441	16.24	4.16						99.4											5.50	
1046	Gomp no const	2.197	0.632	7.3595							99.6											3.41	
1047	Gomp with const	1.345	1.407	6.38	2.953						99.6											5.50	
1048	Spline	5.002	0.6947	4.51								3.252	3.697	2.632	4.498							5.50	1.9
1049	Gomp no const	1.518	0.5347	7.264							99.4											3.41	
1050	Gomp no const	3.056	0.5316	4.261																		1.92	
1051	Gomp no const	0.7512	1.0336	13.528							99.9											5.50	
1052	Gomp with const	1.703	-2.687	866.7	-860.1						98.9											5.50	
1053	Gomp with const	0.954	1.511	10.537	2.752						99.9											5.50	
1054	2 points					1.6211	0.9612				100											1.43	
1055	2 points					2.7553	0.2403				100											1.43	
1056	2 points					2.5211	0.9612				100											1.43	
1057	1 point					2.1					100											1.02	
1058	Gomp no const	2.243	0.5409	6.3543							99.2											4.41	
1059	Gomp with const	1.184	1.346	8.72	2.69						99.9											3.41	
1060	Gomp no const	13.17	0.8657	4.801																		1.92	
1061	Gomp with const	3.039	0.954	1.98	3.63						99.9											3.41	
1062	Gomp no const	13.03	0.8312	4.801																		1.92	
1063	Gomp with const	3.269	1.2838	2.432	4.076						99.9											5.50	
1064	Gomp no const	2.085	0.4008	5.4005							99.7											3.41	
1065	Gomp with const	1.071	1.706	11.692	4.227						99.8											5.50	
1066	Gomp with const	5.614	1.362	2.151	4.598						98.6											5.50	

		Equation 1										Equation 2								
		Gompertz Coefficients				Linear Regression Coefficients						Gompertz Coefficients				Linear Regression Coefficients						
Tree-id	Description	B	M	C	A	b_0	b_1	b_2	b_3	b_4	Adjusted R^2	B_1	M_1	C_1	A_1	b_0_1	b_1_1	b_2_1	b_3_1	b_4_1	Adjusted R^2	Max Age	Node
1067	Gomp no const	5.662	0.4213	3																		2.45	
1068	Dead before age 1																						
1069	Gomp no const	11.65	0.8478	4.702							100											2.45	
1070	Gomp with const	0.3048	-11.35	710.4	-689.1						99.9											5.50	
1071	Gomp with const	4.015	-0.4267	515.8	-509.5						95.9											3.41	
1072	Dead before age 1																						
1073	2 points					3.1105	0.4806				100											1.43	
1074	Gomp with const	2.7656	1.3309	3.9707	4.3292						100											5.50	
1075	Gomp no const	0.963	0.274	7.727							97.4											5.50	
1076	Gomp with const	0.9463	1.8882	10.451	4.689						99.9											5.50	
1077	Dead before age 1																						
1078	Gomp no const	1.4323	0.532	7.09							99.8											3.41	
1079	Gomp with const	3.581	-0.7193	905.8	-899.6						99.9											3.41	
1080	Gomp no const	0.8858	0.2975	8.899							99											5.50	
1081	1 point					1.1					100											1.02	
1082	Gomp with const	0.284	-1.11	50.7	-23.8						99.9											5.50	
1083	1 point					2.5					100											1.02	
1084	Gomp no const	1.574	0.296	6.3454							99.2											5.50	
1085	Gomp with const	1.56	-3.209	1170	-1164						99.7											5.50	
1086	Gomp no const	1.454	0.6566	9.389																		1.92	
1087	Gomp with const	5.09	1.3502	1.161	4.0948						98.2											3.41	
1088	Gomp no const	3.73	0.6213	4.518							99.7											2.45	
1089	Gomp no const	10.84	0.784	5.302							100											2.45	
1090	Gomp no const	0.9225	0.9677	14.558							99.8											5.50	
1091	Gomp with const	0.8345	1.7061	9.886	3.341						100											5.50	
1092	Dead before age 1																						
1093	Gomp no const	1.226	-0.073	6.2749							98.6											5.50	
1094	Gomp with const	0.4184	-10.05	1339	-1321						99.8											5.50	
1095	Gomp no const	1.4017	0.8946	11.7813							99.6											5.50	
1096	Gomp with const	0.6066	-8.811	3817	-3802						99.6											5.50	
1097	Gomp no const	3.969	0.6242	6.812							95.2											5.50	
1098	Gomp with const	0.4642	-13.47	11632	-11613						99.5											5.50	
1099	Dead before age 1																						
1100	Gomp with const	1.862	-0.55	71	-63						99.9											5.50	
1101	Gomp no const	1.2576	0.9568	10.803							99.5											5.50	
1102	Gomp with const	2.023	1.4528	3.201	4.923						99.6											5.50	
1103	Gomp no const	3.469	0.8014	3.7092							93											5.50	
1104	Gomp no const	1.49	0.885	8.44							76.8											2.45	
1105	Gomp with const	2.196	0.54	7.2	-0.9						99.3											5.50	
1106	Gomp with const	0.674	-9.802	12007	-11995						98.8											5.50	
1107	Gomp no const	0.8282	1.2757	17.773							99.9											5.50	

		Equation 1										Equation 2									
		Gompertz Coefficients				Linear Regression Coefficients						Gompertz Coefficients				Linear Regression Coefficients							
Tree-id	Description	B	M	C	A	b_0	b_1	b_2	b_3	b_4	Adjusted R^2	B_1	M_1	C_1	A_1	b_0_1	b_1_1	b_2_1	b_3_1	b_4_1	Adjusted R^2	Max Age	Node
1108	Gomp with const	1.907	0.52	9.1	-1.3						99.4											5.50	
1109	Gomp no const	1.187	1.0606	14.351							98.9											4.41	
1110	Gomp with const	1.878	-2.155	1077	-1070						99.6											5.50	
1111	fell over 1.9					2.5658	0.7209				100	1.3347	2.233		2.35	0.988					99.9	5.50	1.9
1112	Gomp no const	1.766	0.9127	8.1344							99.3											5.50	
1113	Dead before age 1																						
1114	Gomp no const	1.2207	0.8453	9.4474							99.5											5.50	
1115	Gomp with const	0.8063	-8.854	20624	-20611						99.6											5.50	
1116	Gomp with const	1.447	-3.695	2461	-2454						99.2											5.50	
1117	Gomp no const	4.109	0.7103	6.392							97											5.50	
1118	Gomp with const	0.5275	-12.2	13540	-13522						98.6											5.50	
1119	Gomp no const	2.3601	0.7446	6.9274							99.9											5.50	
1120	Gomp with const	3.371	1.421	3.0502	4.9354						99.8											5.50	
1121	Gomp no const	0.4766	2.044	29.23							98.8											5.50	
1122	Gomp with const	2.855	1.4367	2.723	4.6005						99.9											3.41	
1123	Gomp with const	2.4386	0.7909	6.421	0.783						100											5.01	
1124	Gomp with const	1.716	1.3081	4.822	4.264						99.9											5.50	
1125	Gomp with const	0.337	-2.22	70	-44						99.9											5.50	
1126	Gomp with const	1.334	-4.254	3737	-3729						98.9											5.50	
1127	Gomp with const	0.407	-14.68	7117	-7100						99.6											5.50	
1128	Gomp no const	0.6123	1.2205	17.136							99.9											5.50	
1129	Gomp with const	1.828	1.5025	4.529	4.608						99.9											5.50	
1130	Gomp with const	2.136	1.3156	5.473	4.372						99.9											5.50	
1131	Gomp with const	1.3539	1.189	6.207	3.745						99.9											5.50	
1132	Gomp no const	2.102	0.301	5.2486							96.6											3.41	
1133	Gomp no const	0.8108	1.0846	16.949							99.8											5.50	
1134	Gomp no const	2.537	0.559	6.408							97.5											2.45	
1135	Gomp with const	0.322	0.01	41.5	-14.8						99.9											5.50	
1136	Gomp no const	4.762	0.6367	4.70523							100											2.45	
1137	Gomp with const	1.0969	1.6078	9.608	3.693						100											5.50	
1138	1 point					2					100											1.02	
1139	Gomp no const	0.58	1.3975	24.03							99.7											5.50	
1140	Gomp with const	3.509	1.3075	2.799	4.523						99.9											3.41	
1141	Gomp with const	1.8861	1.5159	5.1124	4.2039						100											5.50	
1142	Gomp with const	1.766	1.2633	3.725	5.006						99.9											5.01	
1143	Gomp with const	0.433	-3.7	118	-99						99.8											5.50	
1144	Gomp with const	3.942	0.6073	7.758	-1.653						90											5.50	
1145	1 point					6.1					100											1.02	
1146	Gomp no const	0.7224	1.5107	20.469							99.9											5.50	
1147	Gomp with const	0.5257	-10.71	6010	-5994						99.8											5.50	
1148	Gomp no const	1.8601	0.8588	9.6367							99.7											5.50	

		Equation 1										Equation 2								
		Gompertz Coefficients				Linear Regression Coefficients						Gompertz Coefficients				Linear Regression Coefficients						
Tree-id	Description	B	M	C	A	b_0	b_1	b_2	b_3	b_4	Adjusted R^2	B_1	M_1	C_1	A_1	b_0_1	b_1_1	b_2_1	b_3_1	b_4_1	Adjusted R^2	Max Age	Node
1149	Gomp with const	0.3622	-14.48	4738	-4716						99.8											5.50	
1150	Gomp with const	0.4197	-14.32	9810	-9789						99.6											5.50	
1151	Gomp with const	0.64	0.07	31.4	-13.8						99.8											5.50	
1152	Gomp with const	1.526	-3.348	3468	-3460						97											5.50	
1153	Gomp with const	0.3887	-10.93	1858	-1836						99.8											5.50	
1154	Gomp no const	1.1108	0.7007	9.136							99.2											5.50	
1155	Gomp no const	8.772	0.9216	9.202																		1.92	
1156	Gomp with const	0.3244	-11.7	1209	-1185						99.8											5.50	
1157	Gomp with const	2.014	1.465	8.56	3.82						98.8											5.50	
1158	2 points					-0.0158	3.8447				100											1.43	
1159	Gomp with const	0.364	-2.2	68	-45						99.7											5.50	
1160	Gomp no const	2.057	0.9688	12.2458							99.6											5.50	
1161	Dead before age 1																						
1162	Gomp no const	1.775	0.8501	6.6161							99.1											5.50	
1163	Gomp with const	0.4195	-11.77	3666	-3644						99.5											5.50	
1164	2 points					1.2					100											1.92	
1165	Gomp with const	0.691	-6.652	2035	-2021						99.9											5.50	
1166	Gomp with const	0.964	0.677	18.72	-5.18						99.8											5.50	
1167	Dead before age 1																						
1168	Gomp no const	0.9218	1.1799	15.173							99.9											5.50	
1169	Gomp with const	0.364	0.79	42.7	-11.5						99.9											5.50	
1170	Gomp no const	2.796	0.7284	7.2182							97.7											5.50	
1171	Gomp with const	1.042	0.083	26.5	-13.9						99.9											5.50	
1172	Gomp with const	0.2496	-18.82	3391	-3361						99.4											5.50	
1173	Gomp with const	1.519	1.35	8.946	3.292						99.9											5.50	
1174	Gomp with const	0.4055	-13	4896	-4874						99.9											5.50	
1175	Gomp with const	1.338	1.194	8.42	2.5						99.8											5.50	
1176	Gomp with const	0.3413	-4.492	104.2	-84.95						99.9											5.50	
1177	Gomp with const	0.4568	-15.55	30726	-30705						98.8											5.50	
1178	1 point					5.5					100											1.02	
1179	Gomp with const	1.098	0.884	16	-3.22						99.8											5.50	
1180	Gomp with const	2.075	1.207	4.239	2.633						99.6											5.50	
1181	Gomp with const	0.4135	-12.09	3727	-3706						99.8											5.50	
1182	Gomp with const	14.21	1.342	1.7	4.1						100											3.41	
1183	Dead before age 1																						
1184	Gomp with const	0.3485	-15.68	6208	-6184						99.1											5.50	
1185	Gomp no const	0.862	1.0626	15.63							99.4											5.50	
1186	Dead before age 1																						
1187	2 points					-3.3211	8.1701															1.43	
1188	Gomp with const	1.057	-6.118	14091	-14079						98.3											5.50	
1189	Dead before age 1																						

		Equation 1										Equation 2								
		Gompertz Coefficients				Linear Regression Coefficients						Gompertz Coefficients				Linear Regression Coefficients						
Tree-id	Description	B	M	C	A	b_0	b_1	b_2	b_3	b_4	Adjusted R^2	B_1	M_1	C_1	A_1	b_0_1	b_1_1	b_2_1	b_3_1	b_4_1	Adjusted R^2	Max Age	Node
1190	Dead before age 1																						
1191	Gomp with const	1.845	2.1207	8.053	3.299						98.6											5.50	
1192	Dead before age 1																						
1193	Gomp with const	0.3633	-9.083	836.8	-810.7						100											5.50	
1194	Gomp with const	0.4833	-11.77	6478	-6459						99.7											5.50	
1195	Gomp with const	0.473	-12.59	11673	-11648						99.5											5.50	
1196	fell at 1.4					5.2						1.212	1.8084	4.521							98.1	5.50	1.4
1197	Dead before age 1																						
1198	Gomp no const	2.721	0.8514	4.909							98.2											3.41	
1199	Gomp with const	1.605	1.342	8.044	2.2						99.8											5.50	
1200	Gomp with const	0.3457	-14.51	4914	-4885						99.7											5.50	
1201	Gomp no const	1.7273	0.9134	9.003							99.9											5.50	
1202	Gomp with const	0.36	-10.51	1463	-1435						99.6											5.50	
1203	Gomp with const	0.2917	-15.71	2914	-2886						99.9											5.50	
1204	Gomp with const	0.3662	-12.02	2043	-2020						100											5.50	
1205	Gomp with const	0.498	0.47	32.5	-9.5						99.9											5.50	
1206	Gomp with const	0.582	-0.92	50.3	-31.2						99.9											5.50	
1207	Gomp with const	0.5174	-9.361	3255	-3235						99.8											5.50	
1208	Gomp with const	0.711	-0.15	32.2	-16.4						99.7											5.50	
1209	Gomp with const	1.313	0.494	18.2	-7.8						99.8											5.50	
1210	Gomp with const	0.7453	-9.412	28625	-28609						99.8											5.50	
1211	Gomp with const	3.07	1.7005	2.555	5.3111						99.3											5.50	
1212	Gomp with const	0.838	2.003	9.4	4.858						99.7											5.50	
1213	Gomp with const	0.5192	-13.15	23825	-23805						99.2											5.50	
1214	fell at 1.4					5						0.5098	2.345	8.728							98.9	5.50	1.4
1215	Gomp with const	0.6541	-8.665	7423	-7405						99.8											5.50	
1216	Gomp with const	0.5043	-12.88	18849	-18827						99.3											5.50	
1217	Gomp no const	3.971	0.8707	8.3647							99.7											2.45	
1218	Gomp no const	0.777	-0.165	7.372							92.5											5.50	
1219	1 point					4.3					100											1.02	
1220	Gomp no const	0.87	1.4363	23.88							99.8											5.50	
1221	Gomp with const	1.994	1.476	7.712	3.83						99.3											5.50	
1222	Gomp with const	0.448	-1.5	92	-61						99.9											5.50	
1223	Gomp with const	0.709	1.063	20.04	-3.94						99.7											5.50	
1224	Gomp with const	0.572	-12.82	35129	-35111						98.9											5.50	
1225	1 point					1					100											1.02	
1226	Gomp no const	1.587	1.1191	8.05							99.5											5.50	
1227	Gomp with const	0.458	-13.04	10100	-10080						99.8											5.50	
1228	Gomp with const	1.442	-3.719	5158	-5149						95.6											5.50	
1229	Gomp with const	0.312	-4.3	174	-138						99.8											5.50	
1230	1 point					3.5					100											1.02	

		Equation 1										Equation 2								
		Gompertz Coefficients				Linear Regression Coefficients						Gompertz Coefficients				Linear Regression Coefficients						
Tree-id	Description	B	M	C	A	b_0	b_1	b_2	b_3	b_4	Adjusted R^2	B_1	M_1	C_1	A_1	b_0_1	b_1_1	b_2_1	b_3_1	b_4_1	Adjusted R^2	Max Age	Node
1231	Gomp with const	0.496	-1.56	40.3	-25.1						99.9											5.50	
1232	Dead before age 1																						
1233	Spline	5.837	0.7396	6.206								0.009079	332.9	336300000	5.681							5.50	1.9
1234	Gomp with const	2.589	1.3138	3.521	4.391						99.9											5.50	
1235	Gomp with const	0.3132	-14.58	2120	-2099						99.8											5.50	
1236	Dead before age 1																						
1237	Dead before age 1																						
1238	Gomp with const	0.5749	-11.33	10858	-10844						99.8											5.50	
1239	Dead before age 1																						
1240	Gomp with const	1.855	-2.22	802.4	-796.3						96.7											5.50	
1241	Dead before age 1																						
1242	Gomp no const	1.1666	0.7955	9.7281							99.8											5.50	
1243	Gomp no const	7.366	0.8649	6.903																		1.92	
1244	Spline	15.29	1.051	0.3728	3.328							0.01283	142.5	1501								5.50	2.5
1245	Dead before age 1																						
1246	Gomp with const	0.999	1.562	9.42	3.58						99.6											5.50	
1247	Dead before age 1																						
1248	Gomp with const	0.8286	-8.547	14439	-14428						98.5											5.50	
1249	Gomp no const	0.7928	0.8654	13.221							99.6											5.50	
1250	Dead before age 1																						
1251	Gomp with const	1.596	-3.07	2071	-2063						99.4											5.50	
1252	Dead before age 1																						
1253	Gomp with const	0.6828	1.18	14.94	-0.18						100											5.50	
1254	Gomp no const	1.667	0.6375	9.076							99.4											5.50	
1255	Spline	15.29	1.051	0.9924	3.809							0.01283	404.1	1.66E+71	4.886							5.50	2.5
1256	1 point					5.5					100											1.02	
1257	Spline	4.77	0.6473	4.50521							100	0.01283	225.3	9458509	4.288							5.50	2.5
1258	Dead before age 1																						
1259	Gomp no const	0.7798	0.8358	13.589							99.8											5.50	
1260	Gomp with const	2.0804	0.256	9.75	-3.95						100											5.50	
1261	Gomp with const	0.8594	1.0264	12.904							99.8											5.50	
1262	Gomp with const	2.1676	1.0463	4.904	2.806						100											5.50	
1263	Gomp no const	0.011	164	1410							90.1											5.50	
1264	Gomp no const	1.3639	0.4005	8.144							99.7											5.50	
1265	Gomp with const	0.616	-1.48	47	-33						99.5											5.50	
1266	Dead before age 1																						
1267	Dead before age 1																						
1268	Dead before age 1																						
1269	Gomp no const	2.838	0.5825	4.9639							96.8											5.50	
1270	Gomp with const	9.708	1.016	0.1616	1.339						99.7											3.41	
1271	Gomp no const	0.6878	1.2069	14.429							99.7											5.50	

		Equation 1										Equation 2								
		Gompertz Coefficients				Linear Regression Coefficients						Gompertz Coefficients				Linear Regression Coefficients						
Tree-id	Description	B	M	C	A	b_0	b_1	b_2	b_3	b_4	Adjusted R^2	B_1	M_1	C_1	A_1	b_0_1	b_1_1	b_2_1	b_3_1	b_4_1	Adjusted R^2	Max Age	Node
1272	Gomp no const	1.1072	0.9316	10.605							99.1											5.50	
1273	Gomp no const	1.66	0.419	6.528							96.8											5.50	
1274	Spline	3.606	1.691	1.591	3.515						100	0.02243	21.32	22.02								5.50	4.4
1275	Gomp no const	1.77	0.6837	8.7287							99.2											5.50	
1276	Spline	15.29	1.051	0.3722	2.628							0.01283	225.3	9458509	2.788							5.50	2.5
1277	Spline	15.29	1.051	0.8684	3.232							5.316	2.704	4.3								5.50	3.4
1278	Gomp with const	0.3146	-14.39	2359	-2336						99.9											5.50	
1279	1 point					4.6					100											1.02	
1280	Gomp with const	4.113	0.7125	5.282	-0.8685						95.8											5.50	
1281	Dead before age 1																						
1282	Polynomial 4th order					2.4153	-0.2502	0.3444	-0.0934	0.0084	0.9893											5.50	
1283	Spline	3.943	0.5816	6.216							99.8	9.482	3.527	0.3145	6.386							5.50	2.5
1284	Gomp with const	0.4735	-11.51	4362	-4345						99.9											5.50	
1285	Spline	15.29	1.051	0.3722	3.428							0.01283	380.4	3.903E+52	3.961							5.50	2.5
1286	Gomp with const	1.2219	1.562	9.426	3.05						99.9											5.50	
1287	Spline	5.478	0.7645	4.10367							100	13.35	4.551	0.2003	4.1							5.50	3.4
1288	Gomp with const	0.1435	-17.17	426.4	-390.3						100											5.50	
1289	Dead before age 1																						
1290	Dead before age 1																						
1291	Gomp no const	2.189	0.5788	6.7746							99											5.50	
1292	Gomp with const	2.3903	0.8497	4.107	1.394						100											5.50	
1293	Gomp no const	1.687	0.6246	6.648							98.4											3.41	
1294	Gomp no const	1.063	0.9028	9.8845							99.7											5.50	
1295	Gomp with const	1.0118	1.32	10.759	1.64						100											5.50	
1296	Dead before age 1																						
1297	Gomp no const	2.7201	0.4946	5.72433							100											2.45	
1298	Gomp with const	0.2369	-16.97	1548	-1522						99.8											5.50	
1299	Gomp no const	5.685	0.7954	4.107																		1.92	
1300	Gomp with const	5.54	1.002	1.171	3.531						100											5.01	
1301	Gomp no const	1.762	0.5934	6.565							99.7											2.45	
1302	Gomp no const	0.9444	0.8965	10.402							99.7											5.50	
1303	Gomp with const	0.42	-0.66	45.1	-22.5						99.8											5.50	
1304	Gomp no const	6.3896	0.80108	5.90234							100											2.45	
1305	Gomp no const	2.682	0.322	4.4324							98.3											2.45	
1306	Dead before age 1																						
1307	Gomp with const	1.515	1.681	7.107	3.462						99.9											5.50	
1308	Gomp with const	2.297	1.3545	3.35	4.22						99.6											5.50	
1309	Gomp no const	2.044	0.6476	6.376							99.5											3.41	
1310	Gomp with const	1.468	-3.601	2206	-2199						99.8											5.50	
1311	Dead before age 1																						
1312	Gomp with const	1.944	-2.931	4533	-4527						93.4											3.41	

xl

		Equation 1										Equation 2								
		Gompertz Coefficients				Linear Regression Coefficients						Gompertz Coefficients				Linear Regression Coefficients						
Tree-id	Description	B	M	C	A	b_0	b_1	b_2	b_3	b_4	Adjusted R^2	B_1	M_1	C_1	A_1	b_0_1	b_1_1	b_2_1	b_3_1	b_4_1	Adjusted R^2	Max Age	Node
1313	Gomp no const	0.6295	1.3076	17.181							99.8											5.50	
1314	Dead before age 1																						
1315	2 points					1.6211	0.9612				100											1.43	
1316	3 points					1.9675	0.1139				78.6											1.92	
1317	Gomp no const	0.5734	1.4723	18.895							99.5											5.50	
1318	Gomp with const	1.999	1.2315	4.681	3.688						100											3.41	
1319	Dead before age 1																						
1320	Gomp with const	0.658	-1.67	51	-39						99.9											5.50	
1321	Gomp no const	0.9363	1.1201	13.205							99.8											5.50	
1322	Gomp with const	15.29	1.051	0.8676	2.433																	2.45	
1323	Gomp with const	5.1	1.183	1.672	3.335						99.9											5.50	
1324	Gomp no const	0.5167	1.595	19.53							99											5.50	
1325	Gomp with const	1.553	1.5	7.232	4.169						99.5											5.50	
1326	Dead before age 1																						
1327	2 points					2.1211	0.9612				100											1.43	
1328	Gomp with const	2.4513	0.9963	3.105	2.396						100											5.50	
1329	Gomp no const	0.6246	1.5476	21.501							99.5											5.50	
1330	2 points					2.9105	0.4806				100											1.43	
1331	Gomp with const	3.409	1.3938	2.5596	4.0293						99.9											3.41	
1332	Gomp with const	1.259	1.528	7.888	3.454						99.8											5.50	
1333	2 points					2.5105	0.4806				100											1.43	
1334	Gomp no const	2.616	0.036	4.3167							98.3											2.45	
1335	Gomp with const	0.3772	-11.17	1377	-1359						99.8											5.50	
1336	Gomp with const	1.631	-2.941	1189	-1183						99.4											5.50	
1337	1 point					1.5					100											1.02	
1338	Gomp with const	1.653	1.2292	4.387	3.738						99.9											3.41	
1339	Spline	5.698	0.8232	6.8066							100	0.01283	379.4	7.92E+51	6.96							5.50	2.5
1340	Gomp no const	0.962	1.1997	13.993							98.8											5.50	
1341	Gomp with const	1.252	-0.59	39	-30						99.7											5.50	
1342	Gomp no const	0.8585	1.0821	15.486							99.9											5.50	
1343	Dead before age 1																						
1344	Gomp with const	0.3622	-13.02	2133	-2115						99.8											5.50	
1345	Dead before age 1																						
1346	Gomp no const	1.1675	0.9421	11.22							99.2											5.50	
1347	Gomp with const	0.3909	-13.25	4145	-4124						99.4											5.50	
1348	Dead before age 1																						
1349	Spline	6.29	0.88704	6.50494							100	5.099	4.853	0.3114	6.7							5.50	3.4
1350	Gomp no const	1.2881	1.0795	11.4116							99.8											5.50	
1351	1 point					4					100											1.02	
1352	Spline	5.239	0.78856	6.20828							100	5.099	4.853	0.3114	6.4							5.50	3.4
1353	Gomp with const	0.6027	-3.818	210.7	-195.2						100											5.50	

		Equation 1										Equation 2									
		Gompertz Coefficients				Linear Regression Coefficients						Gompertz Coefficients				Linear Regression Coefficients							
Tree-id	Description	B	M	C	A	b_0	b_1	b_2	b_3	b_4	Adjusted R^2	B_1	M_1	C_1	A_1	b_0_1	b_1_1	b_2_1	b_3_1	b_4_1	Adjusted R^2	Max Age	Node
1354	Gomp no const	1.357	1.0135	10.959							99.7											5.50	
1355	Spline	15.29	1.051	1.985	3.917							2.495	4.473	0.6484	6							5.50	3.4
1356	Gomp with const	0.82	0.657	22.5	-5.88						99.8											5.50	
1357	Gomp no const	1.392	0.9966	9.839							99.1											5.50	
1358	Gomp no const	1.111	0.3807	10.0589							99.7											5.50	
1359	Gomp with const	2.418	1.221	4.997	2.427						99.6											5.50	
1360	Gomp with const	0.4082	-14.17	8969	-8946						99.7											5.50	
1361	1 point					4.4					100											1.02	
1362	Gomp with const	0.3709	-11.97	1880	-1861						99.7											5.50	
1363	Gomp with const	1.35	-4.17	4354	-4347						98.6											5.50	
1364	Gomp with const	0.8962	-7.707	14976	-14965						99.9											5.50	
1365	Gomp no const	1.706	0.8209	9.801																		1.92	
1366	Gomp with const	0.4449	-11.96	4936	-4915						99.8											5.50	
1367	1 point					1					100											1.02	
1368	2 points					0.1526	2.403				100											1.43	
1369	Gomp no const	5.88	0.8699	5.165							94.3											2.45	
1370	Gomp with const	0.2852	-15.47	1959	-1936						99.9											5.50	
1371	Gomp with const	2.55	1.5094	5.108	5.273						98.5											5.50	
1372	Gomp no const	3.629	0.6522	6.6504							97.8											2.45	
1373	Gomp no const	1.0738	0.8617	12.061							99.7											5.50	
1374	Spline	15.29	1.051	1.365	3.737							5.738	2.841	5.3							100	5.50	3.4
1375	Gomp no const	0.9475	0.8774	13.0549							99.8											5.50	
1376	Gomp with const	1.2973	1.6549	6.652	5						99.9											5.50	
1377	Gomp no const	0.6668	1.5422	21.043							99.8											5.50	
1378	Gomp no const	1.492	0.3944	5.9368							99.3											3.41	
1379	Dead before age 1																						
1380	Gomp no const	2.227	0.6558	5.7963							99.6											3.41	
1381	Gomp no const	13.4	0.9003	5.402																		1.92	
1382	Gomp no const	1.6648	0.6793	8.5222							99.7											5.50	
1383	Gomp with const	0.2914	-6.684	221.8	-193.7						99.8											5.50	
1384	Gomp no const	2.064	0.1952	4.322																		1.92	
1385	Gomp no const	0.7821	1.1858	17.046							99.6											5.50	
1386	Gomp no const	13.17	0.8657	4.801																		1.92	
1387	Gomp with const	2.082	1.269	4.081	3.75						99.5											5.01	
1388	Gomp no const	0.9707	1.0603	16.458							99.9											5.50	
1389	Gomp no const	1.706	0.6082	8.845							99.3											3.41	
1390	Gomp with const	0.448	0.18	27.3	-8						99.9											5.50	
1391	Gomp with const	1.722	1.62	6.516	4.571						99.3											5.50	
1392	Gomp no const	4.32	0.624	4.921							88.7											2.45	
1393	Gomp with const	0.545	-11.09	11240	-11220						99.8											5.50	
1394	Gomp no const	0.0383	24.2	44							99.3											5.50	

		Equation 1										Equation 2								
		Gompertz Coefficients				Linear Regression Coefficients						Gompertz Coefficients				Linear Regression Coefficients						
Tree-id	Description	B	M	C	A	b_0	b_1	b_2	b_3	b_4	Adjusted R^2	B_1	M_1	C_1	A_1	b_0_1	b_1_1	b_2_1	b_3_1	b_4_1	Adjusted R^2	Max Age	Node
1395	Gomp with const	0.4883	-11.29	5289	-5270						99.8											5.50	
1396	Gomp with const	0.4711	-14.83	22676	-22658						98.6											5.50	
1397	Gomp with const	1.14	0.681	19	-4.98						99.8											5.50	
1398	Dead before age 1																						
1399	Gomp with const	2.336	1.101	4.714	2.901						99.8											5.50	
1400	Gomp with const	0.6676	-9.533	12839	-12822						99.9											5.50	
1401	Gomp with const	0.6256	-8.813	6243	-6224						99.6											5.50	
1402	Gomp with const	1.348	-4.183	4901	-4893						97.3											5.50	
1403	Dead before age 1																						
1404	Gomp with const	2.726	1.496	4.506	3.393						99.8											5.50	
1405	Dead before age 1																						
1406	Gomp with const	0.946	-0.63	61	-46						99.8											5.50	
1407	Dead before age 1																						
1408	Gomp with const	0.3546	-17.15	11909	-11884						98.5											5.50	
1409	Gomp with const	0.47	-13.85	16216	-16196						99.4											5.50	
1410	Dead before age 1																						
1411	Gomp no const	1.0397	1.0223	15.23							99.7											5.50	
1412	Gomp with const	1.088	1.409	10.5	3.37						99.6											5.50	
1413	Gomp with const	0.4073	-12.63	4152	-4130						99.8											5.50	
1414	1 point						1.2				100											1.02	
1415	Gomp with const	0.394	-14.52	7886	-7864						99.7											5.50	
1416	Gomp with const	0.5312	-6.701	708.7	-691.7						99.9											5.50	
1417	Gomp with const	0.917	-0.22	27.2	-14.8						99.8											5.50	
1418	Gomp no const	0.9239	1.2492	17.712							99.7											5.50	
1419	Gomp with const	1.872	-2.171	1409	-1400						99.3											5.50	
1420	Gomp with const	0.4392	-8.248	756.1	-738.4						99.9											5.50	
1421	Gomp with const	1.3473	1.2406	9.276	2.896						100											5.50	
1422	Gomp with const	0.4896	-9.323	2174	-2155						99.8											5.50	
1423	Gomp no const	0.999	1.1887	17.223							98.7											5.50	
1424	Gomp with const	0.3821	-15.28	8420	-8398						99.7											5.50	
1425	Gomp with const	1.125	-0.11	36.7	-23.3						99.6											5.50	
1426	1 point						1.1				100											1.02	
1427	Gomp no const	1.1891	1.0166	13.803							99.7											5.50	
1428	Gomp no const	2.2872	0.79572	6.9303							100											3.41	
1429	Gomp with const	0.8296	-8.534	30249	-30235						99.6											5.50	
1430	fell at 1.4						4.2					3.9011	1.63337	2.4838	1.7168						100	5.50	1.4
1431	Dead before age 1																						
1432	Gomp with const	0.83	0.65	25.5	-7.9						99.7											5.50	
1433	Gomp with const	0.841	1.001	21.66	-4.97						99.6											5.50	
1434	Gomp with const	0.72	-1.13	70	-52						99.8											5.50	
1435	Gomp with const	0.662	-8.168	5159	-5142						100											5.50	

		Equation 1										Equation 2								
		Gompertz Coefficients				Linear Regression Coefficients						Gompertz Coefficients				Linear Regression Coefficients							
Tree-id	Description	B	M	C	A	b_0	b_1	b_2	b_3	b_4	Adjusted R^2	B_1	M_1	C_1	A_1	b_0_1	b_1_1	b_2_1	b_3_1	b_4_1	Adjusted R^2	Max Age	Node
1436	Gomp with const	0.4016	-5.231	217.6	-197						99.9											5.50	
1437	Gomp no const	1.8478	1.1016	9.7451							99.7											5.50	
1438	Gomp with const	0.6171	-9.114	7214	-7197						99.8											5.50	
1439	Gomp with const	0.3229	-17.79	9007	-8982						99.5											5.50	
1440	Gomp no const	0.8163	1.2606	16.945							99.8											5.50	
1441	Gomp with const	1.811	1.227	5.744	2.971						99.9											5.50	
1442	Gomp with const	0.45	-4.58	185.1	-166						99.4											5.50	
1443	Gomp with const	1.329	-4.285	6782	-6771						98.5											5.50	
1444	Gomp no const	3.788	0.8005	7.1463							97.2											5.50	
1445	Gomp with const	0.5975	-7.62	1708	-1693						100											5.50	
1446	Gomp with const	0.9438	1.507	13.68	2.87						99.9											5.50	
1447	Gomp with const	1.739	1.162	7.516	3.027						99.9											5.50	
1448	Spline	0.978	1.107	18.47							98.8	6.111	4.789	4.256	16.7							5.50	3.4
1449	Gomp with const	0.397	-2.47	86	-62						99.9											5.50	
1450	Gomp no const	1.6463	0.8406	11.1893							99.9											5.50	
1451	Gomp with const	0.6217	0.097	31.6	-11.4						99.9											5.50	
1452	Gomp no const	1.0351	1.091	17.87							99.8											5.01	
1453	Gomp with const	0.3616	-13.54	2857	-2837						99.9											5.50	
1454	Gomp with const	0.3391	-11.02	1418	-1389						99.9											5.50	
1455	Gomp no const	1.1143	0.8659	11.995							99.2											5.50	
1456	Gomp with const	0.467	-2.16	73	-53						99.9											5.50	
1457	Gomp no const	1.0486	0.7768	13.234							99.6											5.50	
1458	Gomp no const	0.63	1.4942	26.491							99.9											5.50	
1459	2 points					2.7526	2.403				100											1.43	
1460	Gomp with const	0.311	-16.86	6621	-6591						99.4											5.50	
1461	Dead before age 1																						
1462	Spline	17.67	1.444	1.3	2.7							0.285	3.96	12.91							99.6	5.50	3.4
1463	Dead before age 1																						
1464	Gomp no const	1.186	1.272	20.08																		1.92	
1465	Gomp with const	0.699	-3.4	290	-271						99.1											5.50	
1466	Gomp with const	1.271	1.654	7.192	3.704						99.5											5.50	
1467	Gomp with const	0.4076	-14.1	10079	-10052						99.5											5.50	
1468	Gomp with const	0.819	1.718	11.63	3.36						99.6											5.50	
1469	Gomp with const	1.378	-4.026	5672	-5661						99											5.50	
1470	Gomp no const	0.9456	1.3682	17.599							99.7											5.50	
1471	Gomp with const	1.113	1.7994	18.07	3.74						99.8											5.50	
1472	Gomp with const	0.7281	-10.07	30045	-30031						99.6											5.50	
1473	Gomp with const	0.3429	-15.07	5449	-5422						99.8											5.50	
1474	1 point					4.1					100											1.02	
1475	Gomp with const	4.13	1.419	6.376	3.472						90.4											5.50	
1476	Gomp no const	1.7779	1.228	10.6962							99.9											5.50	

Appendix 4: Coefficients derived for use with the Gompertz function to model mean basal area per plot

Plot-ID	Genotype	Planting Density	Rep	B	C	M
1	Clone	6667	1	0.698	0.007982	1.676
2	Seedling	6667	1	0.5176	0.01555	2.558
3	Clone	3333	1	0.711	0.011449	1.779
4	Seedling	3333	1	0.5037	0.01854	2.63
5	Clone	2222	1	0.734	0.01716	1.9208
6	Seedling	2222	1	0.7134	0.018756	2.2452
7	Clone	1587	1	0.7346	0.017371	2.0264
8	Seedling	1587	1	0.691	0.02882	2.2502
9	Clone	1111	1	0.6191	0.03417	2.3565
10	Seedling	1111	1	0.6412	0.03306	2.4815
11	Clone	6667	2	0.751	0.008505	1.666
12	Seedling	6667	2	0.505	0.01192	2.329
13	Clone	3333	2	0.7092	0.013406	1.877
14	Seedling	3333	2	0.5909	0.01651	2.243
15	Clone	2222	2	0.7609	0.016843	1.8786
16	Seedling	2222	2	0.7505	0.018702	2.045
17	Clone	1587	2	0.6573	0.023031	2.1945
18	Seedling	1587	2	0.5951	0.03068	2.5796
19	Clone	1111	2	0.6107	0.03442	2.4679
20	Seedling	1111	2	0.6841	0.032017	2.328
21	Clone	6667	3	0.647	0.007445	1.585
22	Seedling	6667	3	0.517	0.01303	2.419
23	Clone	3333	3	1.106	0.00995	1.477
24	Seedling	3333	3	0.6396	0.019415	2.332
25	Clone	2222	3	0.7471	0.017672	1.8196
26	Seedling	2222	3	0.6915	0.027043	2.2576
27	Clone	1587	3	0.6624	0.025536	2.2514
28	Seedling	1587	3	0.634	0.022736	2.1777
29	Clone	1111	3	0.7444	0.029176	2.1391
30	Seedling	1111	3	0.824	0.025153	2.1967
41	Clone	6667	5	0.762	0.007736	1.514
42	Seedling	6667	5	0.4242	0.01688	3.039
43	Clone	3333	5	0.959	0.009079	1.5167
44	Seedling	3333	5	0.4327	0.02475	2.988
45	Clone	2222	5	0.7072	0.020018	2.1763
46	Seedling	2222	5	0.6056	0.02225	2.394
47	Clone	1587	5	0.6567	0.025022	2.2807
48	Seedling	1587	5	0.6106	0.02685	2.4659
49	Clone	1111	5	0.728	0.023104	2.1716
50	Seedling	1111	5	0.6473	0.03291	2.5156
51	Clone	6667	6	0.676	0.008522	1.679
52	Seedling	6667	6	0.5	0.01601	2.729
53	Clone	3333	6	0.811	0.012443	1.8027
54	Seedling	3333	6	0.5232	0.02196	2.711
55	Clone	2222	6	0.7736	0.018677	1.9708
56	Seedling	2222	6	0.7668	0.020406	2.0205
57	Clone	1587	6	0.8277	0.018741	2.0672
58	Seedling	1587	6	0.7021	0.024941	2.1079
59	Clone	1111	6	0.6214	0.02854	2.4403
60	Seedling	1111	6	0.921	0.020482	1.9784

Appendix 5: Coefficients derived for use with the Gompertz function to model mean dominant basal area per plot

				Gompertz function coefficients			
Plot-id	**Spp**	**Stock**	**Rep**	**A**	**B**	**C**	**M**
1	Clone	6667	1	-0.00501	0.3998	0.04563	2.4797
2	Seedling	6667	1	-0.002116	0.388	0.04367	3.1286
3	Clone	3333	1	-0.00506	0.4348	0.04304	2.3233
4	Seedling	3333	1	-0.000882	0.5651	0.03941	2.7191
5	Clone	2222	1	-0.00614	0.5379	0.03977	1.811
6	Seedling	2222	1	-0.00539	0.5076	0.04559	2.2592
7	Clone	1587	1	-0.003837	0.5327	0.037	2.304
8	Seedling	1587	1	-0.00443	0.4688	0.05729	2.5308
9	Clone	1111	1	-0.00871	0.4788	0.05718	2.0325
10	Seedling	1111	1	-0.003204	0.4926	0.06246	2.8022
11	Clone	6667	2	-0.002052	0.4498	0.04132	2.9561
12	Seedling	6667	2	0.000025	0.5472	0.04089	2.902
13	Clone	3333	2	-0.00526	0.4165	0.04419	2.4087
14	Seedling	3333	2	-0.00502	0.3788	0.05295	2.7918
15	Clone	2222	2	-0.01285	0.383	0.05292	1.658
16	Seedling	2222	2	-0.00525	0.4289	0.05346	2.5623
17	Clone	1587	2	-0.00591	0.4788	0.05084	2.3099
18	Seedling	1587	2	-0.0045	0.481	0.05759	2.4416
19	Clone	1111	2	-0.00715	0.4557	0.06484	2.4543
20	Seedling	1111	2	-0.005857	0.427	0.06849	2.8301
21	Clone	6667	3	-0.00355	0.4146	0.03919	2.6298
22	Seedling	6667	3	-0.00552	0.3587	0.05848	2.9275
23	Clone	3333	3	-0.00596	0.4479	0.04801	2.2618
24	Seedling	3333	3	-0.00282	0.5279	0.04401	2.4165
25	Clone	2222	3	-0.00602	0.465	0.04473	2.094
26	Seedling	2222	3	-0.003485	0.5282	0.05681	2.4824
27	Clone	1587	3	-0.0069	0.4798	0.05261	2.1434
28	Seedling	1587	3	-0.00333	0.5218	0.04787	2.262
29	Clone	1111	3	-0.00691	0.5966	0.04344	1.7601
30	Seedling	1111	3	-0.003069	0.7382	0.039398	2.0156
41	Clone	6667	5	-0.00498	0.39	0.04151	2.414
42	Seedling	6667	5	-0.000665	0.4357	0.03887	3.1773
43	Clone	3333	5	-0.002447	0.663	0.02788	1.9247
44	Seedling	3333	5	-0.001071	0.4781	0.05473	3.0078
45	Clone	2222	5	-0.00458	0.4553	0.04333	2.462
46	Seedling	2222	5	-0.00465	0.3957	0.06132	2.9589
47	Clone	1587	5	-0.00691	0.4835	0.05325	2.1675
48	Seedling	1587	5	-0.00667	0.4369	0.06443	2.5508
49	Clone	1111	5	-0.002472	0.7207	0.03944	2.0967
50	Seedling	1111	5	-0.00637	0.4768	0.07006	2.6097
51	Clone	6667	6	-0.00467	0.4306	0.03519	2.217
52	Seedling	6667	6	-0.00202	0.4504	0.04416	2.9034
53	Clone	3333	6	-0.00447	0.5634	0.03508	1.9734
54	Seedling	3333	6	-0.002887	0.5136	0.04287	2.4662
55	Clone	2222	6	-0.00747	0.5476	0.04182	1.706
56	Seedling	2222	6	-0.00543	0.4812	0.04163	2.114
57	Clone	1587	6	-0.00553	0.5121	0.03835	2.0957
58	Seedling	1587	6	-0.249	0.1249	0.354	-7.6
59	Clone	1111	6	-0.0091	0.4789	0.05696	2.0197
60	Seedling	1111	6	-0.000565	0.7928	0.036003	2.2729